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TRANSMITTAL LETTER TO THE UNITED STATES DESIGNATED/ELECTED OFFICE (DO/EO/US) CONCERNING A FILING UNDER 35 U.S.C. 371

ATTORNEY'S DOCKET NUMBER: 001560-350

U S APPLICATION NO (If known, see 37 C F R 1.5): Unassigned 09/147955

INTERNATIONAL APPLICATION NO.	INTERNATIONAL FILING DATE	PRIORITY DATE CLAIMED
PCT/JP98/03199	16 July 1998	25 July 1997

TITLE OF INVENTION
GENE CODING FOR A PROTEIN HAVING GLYCOSIDE TRANSFER ACTIVITY

APPLICANT(S) FOR DO/EO/US
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Applicant herewith submits to the United States Designated/Elected Office (DO/EO/US) the following items and other information:

1. ☒ This is a **FIRST** submission of items concerning a filing under 35 U.S.C. 371.
2. ☐ This is a **SECOND** or **SUBSEQUENT** submission of items concerning a filing under 35 U.S.C. 371.
3. ☒ This is an express request to begin national examination procedures (35 U.S.C. 371(f)) at any time rather than delay examination until the expiration of the applicable time limit set in 35 U.S.C. 371(b) and the PCT Articles 22 and 39(1).
4. ☐ A proper Demand for International Preliminary Examination was made by the 19th month from the earliest claimed priority date.
5. ☒ A copy of the International Application as filed (35 U.S.C. 371(c)(2))
   a. ☐ is transmitted herewith (required only if not transmitted by the International Bureau).
   b. ☒ has been transmitted by the International Bureau.
   c. ☐ is not required, as the application was filed in the United States Receiving Office (RO/US)
6. ☒ A translation of the International Application into English (35 U.S.C. 371(c)(2)).
7. ☒ Amendments to the claims of the International Application under PCT Article 19 (35 U.S.C. 371(c)(3))
   a. ☐ are transmitted herewith (required only if not transmitted by the International Bureau).
   b. ☐ have been transmitted by the International Bureau.
   c. ☐ have not been made; however, the time limit for making such amendments has NOT expired.
   d. ☒ have not been made and will not be made.
8. ☐ A translation of the amendments to the claims under PCT Article 19 (35 U.S.C. 371(c)(3)).
9. ☒ An oath or declaration of the inventor(s) (35 U.S.C. 371(c)(4)).
10. ☐ A translation of the annexes to the International Preliminary Examination Report under PCT Article 36 (35 U.S.C. 371(c)(5)).

Items 11. to 16. below concern other document(s) or information included:

11. ☒ An Information Disclosure Statement under 37 CFR 1.97 and 1.98.
12. ☒ An assignment document for recording. A separate cover sheet in compliance with 37 CFR 3.28 and 3.31 is included.
13. ☒ A FIRST preliminary amendment.
    ☐ A SECOND or SUBSEQUENT preliminary amendment.
14. ☐ A substitute specification.
15. ☐ A change of power of attorney and/or address letter.
16. ☒ Other items or information:

    Copy of International Search Report, and a copy of Notice Informing Applicant of the Communication of the International Application to the Designated Offices.

(10/97)

U.S. APPLICATION NO. (If known, see 37 C.F.R. 1.50) Unassigned	INTERNATIONAL APPLICATION NO. PCT\JP 98\03199	ATTORNEY'S DOCKET NUMBER 001560-350

17. [x] The following fees are submitted:	CALCULATIONS	PTO USE ONLY
Basic National Fee (37 CFR 1.492(a)(1)-(5)):		
Search Report has been prepared by the EPO or JPO $840.00		
International preliminary examination fee paid to USPTO (37 CFR 1.482) $670.00		
No international preliminary examination fee paid to USPTO (37 CFR 1.482) but international search fee paid to USPTO (37 CFR 1.445(a)(2)) $760.00		
Neither international preliminary examination fee (37 CFR 1.482) nor international search fee (37 CFR 1.445(a)(2)) paid to USPTO $970.00		
International preliminary examination fee paid to USPTO (37 CFR 1.482) and all claims satisfied provisions of PCT Article 33(2)-(4) $96.00		
ENTER APPROPRIATE BASIC FEE AMOUNT =	$ 840.00	
Surcharge of **$130.00** for furnishing the oath or declaration later than ☐ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492(e)).	$	

Claims	Number Filed	Number Extra	Rate		
Total Claims	19 -20 =	0	X$18.00	$ 0.00	
Independent Claims	1 -3 =	0	X$78.00	$ 0.00	
Multiple dependent claim(s) (if applicable)			+$260.00	$ 0.00	
TOTAL OF ABOVE CALCULATIONS =				$ 840.00	
Reduction for 1/2 for filing by small entity, if applicable. Verified Small Entity statement must also be filed. (Note 37 CFR 1.9, 1.27, 1.28).				$ 0.00	
SUBTOTAL =				$ 840.00	
Processing fee of **$130.00** for furnishing the English translation later than ☐ 20 ☐ 30 months from the earliest claimed priority date (37 CFR 1.492(f)). +				$ 0.00	
TOTAL NATIONAL FEE =				$ 840.00	
Fee for recording the enclosed assignment (37 CFR 1.21(h)). The assignment must be accompanied by an appropriate cover sheet (37 CFR 3.28, 3.31). $40.00 per property +				$ 40.00	
TOTAL FEES ENCLOSED =				$ 880.00	
				Amount to be: refunded	$
				charged	$

a. [x] A check in the amount of $ 880.00 to cover the above fees is enclosed.

b. ☐ Please charge my Deposit Account No. 02-4800 in the amount of $_____ to cover the above fees. A duplicate copy of this sheet is enclosed.

c. [x] The Commissioner is hereby authorized to charge any additional fees which may be required, or credit any overpayment to Deposit Account No. 02-4800. A duplicate copy of this sheet is enclosed.

NOTE: Where an appropriate time limit under 37 CFR 1.494 or 1.495 has not been met, a petition to revive (37 CFR 1.137(a) or (b)) must be filed and granted to restore the application to pending status.

SEND ALL CORRESPONDENCE TO:

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SIGNATURE

Donna M. Meuth
NAME

36,607
REGISTRATION NUMBER

(10/97)

Patent
Attorney's Docket No. 001560-350

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of	)	
	)	
Masako MIZUTANI et al	)	Group Art Unit: Unassigned
	)	
Application No.: Unassigned Corresponding to PCT/JP 98/03199	)	Examiner: Unassigned
	)	
Filed: March 24, 1999	)	
	)	
For: GENE CODING FOR A PROTEIN HAVING GLYCOSIDE TRANSFER ACTIVITY	)	

PRELIMINARY AMENDMENT

Assistant Commissioner for Patents
Washington, D.C. 20231

Sir:

Prior to examination on the merits, please amend the above identified application as follows:

IN THE SPECIFICATION:

In compliance with 37 C.F.R. § 1.823(a), please substitute the attached copy of the "Sequence Listing" for the current "Sequence Listing" at pages 22-39 of the above-identified application.

IN THE CLAIMS:

Please amend claims 6, 8 and 10 as follows:

In claim 6, lines 1 and 2, please delete "any one of claims 1 through 5" and insert therefore --claim 1--.

In claim 8, lines 1 and 2, please delete "any one of claims 1 through 5" and insert therefore --claim 1--.

In claim 10, line 2, please delete "any one of claims 1 through 5" and insert therefore --claim 1--.

Please insert the following new claims 12-19 as follows:

--12. A protein encoded by a gene as set forth in claim 2.

13. A protein encoded by a gene as set forth in claim 3.

14. A protein encoded by a gene as set forth in claim 4.

15. A protein encoded by a gene as set forth in claim 5.

16. A plant into which is introduced a gene as set forth in claim 2, or its progeny or tissue having identical properties.

17. A plant into which is introduced a gene as set forth in claim 3, or its progeny or tissue having identical properties.

18. A plant into which is introduced a gene as set forth in claim 4, or its progeny or tissue having identical properties.

19. A plant into which is introduced a gene as set forth in claim 5, or its progeny or tissue having identical properties.--

REMARKS

Entry of the foregoing and examination of the above-identified application is respectfully requested.

The paper copy of the Sequence Listing for the subject application, is by this amendment, substituted for the current Sequence Listing at pages 22-39 and before the claims of the above-identified application. Please renumber the pages accordingly.

Claims 6, 8 and 10 have been amended to eliminate the multiple dependency of the claims and to place them in better form in accordance with U.S. practice. New claims 12-19 have been added directed to preferred embodiments. Support for these claims may be found at the very least in original claims 8 and 10.

Early and favorable action in the form of Notice of Allowance is respectfully requested.

In the event that there are any questions relating to this amendment or the application in general, it would be appreciated if the Examiner would contact the undersigned attorney be telephone so that prosecution would be expedited.

Respectfully submitted,

BURNS, DOANE, SWECKER & MATHIS, L.L.P.

By: _____
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Date: March 24, 1999

SPECIFICATION

GENE CODING FOR A PROTEIN HAVING GLYCOSIDE TRANSFER ACTIVITY

Technical Field

The present invention relates to a gene coding for a protein having activity that transfers a glycoside to the 5 position of a flavonoid, and a process utilizing that gene.

Background Art

The flower industry strives to develop various new varieties. Changing the color of a flower is one way of effectively breeding a new variety. A wide range of colors have been successfully produced for nearly all commercial varieties using classical breeding methods. With these methods, however, since there are restrictions on the gene pool for each species, it is rare for a single species to have a broad range of colored varieties.

Flower colors are based on two types of pigments, namely flavonoids and carotinoids. Flavonoids contribute to color tones ranging from yellow to red and blue, while carotinoids contribute to color tones of orange or yellow. Flavonoid molecules that primarily contribute to flower color are anthocyanins which are glycosides of cyanidin, delphinidin, petunidin, peonidin, malvidin and pelargonidin, and different anthocyans cause remarkable changes in flower color. Moreover, flower color is also affected by auxiliary coloring by colorless flavonoids, metal complex formation, glucosylation, acylation, methylation and vacuolar pH (Forkmann, Plant Breeding, 106, 1, 1991).

The biosynthesis route of anthocyanins, which begins with phenylalanine, has been well understood (e.g., Plant Cell, 7, 1071-1083, 1995), and nearly all genes involved in the biosynthesis have been cloned. For example, among those genes thought to be involved in biosynthesis of

malonylshisonin (3-O-(6-O-(p-cumaloyl)-β-D-glucosyl)-5-O-(6-O-malonyl-β-D-glucosyl)-cyanidin), which is an anthocyanin of Perilla, those genes for which homologues have not yet been reported are only the flavonoid-3'-hydroxylase, UDP-glucose:anthocyanin (flavonoid) 5-O-glucosyl transferase (abbreviated as 5GT) and malonyl group transferase genes.

Among these, flavonoid-3'-hydroxylase is known to belong to the cytochrome P450 gene family (Plant Cell, 7, 1071-1083, 1995), and cytochrome P450 genes are surmised to demonstrate structural homology.

The hydroxyl group at the 3 position of flavonoid molecules is typically modified by glucose, and generally glucosylation and other modifications by glycoside are considered to increase the stability and solubility of anthocyanins (The Flavonoids, Chapman & Hall, 1994).

Genes coding for the UDP-glucose:anthocyanidin or flavonoid-3-glucosyl transferase (abbreviated as 3GT) that catalyze this reaction are obtained from numerous plants such as corn, barley, snapdragons and gentians, and their amino acid sequences mutually demonstrate significant homology. For example, the homology between the 3GT amino acid sequences of monocotyledonous corn and dicotyledoneous gentian is 32%, that between the 3GT amino acid sequences of monocotyledonous corn and monocotyledonous barley is 73%, and that between the 3GT amino acid sequences of dicotyledonous gentian and dicotyledonous eggplant is 46%.

In addition, the gene coding for UDP-ramnose:anthocyanidin 3-glucosidoramnosyl transferase (3RT) of petunias has also been cloned.

However, even though the hydroxyl group at the 5 position of the flavonoids of numerous plants is glucosylated, a gene for the enzyme (5GT) that catalyzes this reaction has yet to be obtained.

In addition, although there are examples of measuring the reaction by which glycoside is transferred to the 5

position of petunia and stock anthocyanins (Planta, 160, 341-347, 1984, Planta, 168, 586-591, 1986), these reports only describe the investigation of enzymological properties using crude extracts or partially purified products of flower petals, and there are no examples of this enzyme being purified to its pure form. In addition, since glycosyltransferases are typically biochemically unstable, enzyme purification is difficult.

Although there are hardly any cases in which color tone is changed by addition of glycoside to a flavonoid molecule, since aromatic acyl groups that have a significant effect on color tone are linked to a glucose molecule or ramnose molecule within an anthocyanin, regulation of the glycoside transfer reaction is important in terms of controlling anthocyanin biosynthesis, and ultimately in controlling flower color. Furthermore, as an example of changing flower color by regulating the expression of glycosyltransferase gene, the reaction by petunia 3RT has been controlled in transformed petunia to modify flower color.

Plant species, which can be transformed with a foreign gene, include, for example, roses, chrysanthemums, carnations, daisies, petunias, torenia, bellflowers, calanchoes, tulips and gladiolas.

Disclosure of the Invention

The inventors of the present invention therefore sought to obtain a gene that codes for a protein having activity that transfers a glycoside to the 5 position of a flavonoid, thereby leading to completion of the present invention.

For example, the 5 position hydroxyl group of the anthocyanins of chrysanthemums and some of the anthocyanins of roses and carnations are not glucosylated. The anthocyanin structure can be changed by introducing the 5GT gene obtained by the present invention into these plants.

In addition, although it is possible to change flower color and stabilize flavonoids by acylating flavonoids using the acyl group transferase gene described in International Publication No. WO96/25500, since the acyl group does not bond directly with the flavonoid, but rather bonds by way of a sugar, simply introducing an acyl group transferase gene alone is not sufficient for changing flower color and may even cause the flavonoid not to become stable.

However, by introducing the 5GT gene in combination with an acyl group transferase gene, sugar is bounded to the 5 position of the flavonoid thereby further allowing the flavonoid to be acylated. This can be expected to change the anthocyanin structure and cause the flower color to become bluish.

In addition, if expression of 5GT gene of a plant in which the 5 position of anthocyanin is glucosylated is suppressed with the antisense method or co-suppression method and so forth, transfer of glucose residue to 5 position can be inhibited. So that, flower color can be changed. For example, suppressing 5GT activity in gentian or bellflower can be expected to cause flower color to become reddish.

The inventors of the present invention isolated cDNA of 5GT from Perilla, torenia, verbena and petunia plants using gene recombination technology, and determined the nucleotide sequence of the structural gene. Namely, the inventors of the present invention provide a DNA sequence that codes for 5GT present in the tissue that expresses anthocyanins in these plants. Moreover, since this enzyme transfers glycoside to the 5 position of anthocyanin pigment, it can be used to change flower color and increase anthocyanin stability.

Embodiment for Carrying Out the Invention

The method of differential displacement, for example, can be used to obtain DNA that codes for the enzyme of the

present invention. In Perilla (Perilla frutescens), for example, there are varieties that accumulate anthocyanins (e.g., red forma) and those that do not (e.g., green forma). By cloning DNA present in varieties that accumulate anthocyanins but not present in varieties that do not, it is possible to obtain the DNA that codes for the enzyme of the present invention.

More specifically, RNA is extracted from the leaves of red forma and green forma, and cDNA is synthesized in accordance with standard methods. This is then separated by electrophoresis to isolate cDNA present in the cDNA library of red forma but not present in the cDNA library of green forma. Next, the red forma cDNA library is screened using the resulting cDNA as a probe to obtain the cDNA that codes for the enzyme of the present invention.

Once cDNA that codes for the enzyme of the present invention is obtained in the manner described above, this cDNA or its fragment is used as a probe to screening the cDNA libraries of other plants. As a result, the DNA that codes for the enzyme of the present invention can be obtained from those plants.

As an example of the screening, in the present invention, the DNA coding for the enzyme of the present invention is cloned from Perilla by the differential display method (Example 1). Next, DNA that codes for the enzyme of the present invention is obtained from verbena by screening of cDNAs from verbena (Verbena hybrida) using the cloned DNA of Example 1 as a probe (Example 2). Moreover, DNA coding for the enzyme of the present invention is obtained from torenia in the same manner (Example 3).

Then, it was confirmed that the proteins encoded in these DNAs have the enzymatic activity of the present invention.

Moreover, the DNA coding for the enzyme of the present invention was obtained from petunia (Example 4).

Examples of the DNAs of the present invention include

that which codes for the amino acid sequence described in any one of SEQ ID NOs: 7 through 10 or 12. However, proteins having an amino acid sequence modified by addition and/or deletion of one or more amino acids and/or substitutions by one or more other amino acids are also known to maintain enzymatic activity similar to the original protein. Thus, genes coding for a protein that has an amino acid sequence modified by addition and/or deletions of one or more amino acids and/or substitutions by one or more other amino acids relative to the amino acid sequence described in any one of SEQ ID NOs: 7 through 10 or 12, and still maintains activity of transferring a glycoside to the 5 position of a flavonoid, also belong to the present invention.

The present invention also relates to a gene coding for a protein which gene hybridizes to a nucleotide sequence described in any one of SEQ ID NOs: 1 through 4 or 6, or to a nucleotide sequence that codes for an amino acid sequence described therein or to their portions, for example a portion coding for at least six amino acids of a consensus region, under conditions of 2 to 5 x SSC, and for example, 5 x SSC, and 50°C, and that has activity of transferring a glycoside to the 5 position of a flavonoid. Furthermore, the optimum hybridization temperature varies according to the nucleotide sequence and its length, and it is preferable that the hybridization temperature be lower the shorter the nucleotide sequence. For example, a temperature of 50°C or lower is preferable in the case of a nucleotide sequence (18 bases) coding for six amino acids.

Although examples of genes selected by hybridization in this manner include those which are naturally-occurring such as those derived from plants, examples of which include a gene derived from verbena and torenia, they may also be those derived from other plants, examples of which include petunias, roses, carnations and hyacinths. In addition, genes selected by hybridization may also be cDNA or genomic DNA.

Moreover, the present invention also relates to a gene coding for a protein having an amino acid sequence having homology of 30% or more, preferably 50% or more, for example 60% or 70% or more, and in some cases, 90% or more relative to an amino acid sequence of any of SEQ ID NOs: 7 through 10 or 12, and having activity that transfers a glycoside to the 5 position of a flavonoid. Namely, as indicated in Examples, DNA coding for the enzyme of the present invention demonstrates homology of 20 to 30% in comparison with other glycosyltransferase genes. Thus, the present invention includes genes coding for a protein that having homology of 30% or more with an amino acid sequence described in any one of SEQ ID NOs: 7 through 10 or 12, and has glycosyltransferase activity.

In addition, as is clear from a comparison of the results of Examples 1 through 4, the amino acid sequence of the enzyme of the present invention varies according to the species, with interspecies homology being 50% or more (see Examples 3 and 4), and for example 60 to 70% (see Example 2), while the homology of the amino acid sequences of the enzymes derived from the same species is 90% or more (see Example 1). Thus, genes coding for a protein that has an amino acid sequence having homology of 50% or more, for example 60-70% or more, and in some cases, 90% or more, relative to an amino acid sequence described in any one of SEQ ID NOs: 7 through 10 or 12, and maintains the glycosyltransferase activity of the present invention are included in the present invention.

As is described in detail in Examples, DNA having a native nucleotide sequence is obtained by, for example, screening of a cDNA library.

In addition, DNA coding for an enzyme having a modified amino acid sequence can be synthesized using ordinary site-specific mutagenesis and PCR based on the nucleotide sequence of a native DNA. For example, a DNA fragment containing a site at which a modification is desired to be introduced is obtained by restriction enzyme

digestion of cDNA or genomic DNA obtained as described above. By using this as a template, site-specific mutagenesis or PCR is performed using a primer containing the desired mutation to obtain a DNA fragment containing the desired modification. This is then ligated to DNA coding for another portion of the target enzyme.

Alternatively, in order to obtain DNA coding for an enzyme having a shortened amino acid sequence, for example, DNA coding for an amino acid sequence that is longer than the target amino acid sequence, for example that coding for the entire amino acid sequence, is digested by a desired restriction enzyme, and in the case the resulting DNA fragment does not code for the entire target amino acid sequence, the deficient portion should be supplemented by ligating synthetic DNA.

In addition, by expressing this clone using a gene expression system in E. coli or yeast and measuring enzyme activity, the resulting gene can be confirmed to code for glycosyltransferase, and by clarifying the translation region of glycosyltransferase gene that transfers glycoside to the 5 position of a flavonoid, a gene is obtained that codes for the glycosyltransferase claimed in the present invention. Moreover, by expressing said gene, the target transferase protein that transfers a glycoside to the 5 position of a flavonoid can be obtained.

Alternatively, the protein can be obtained by using antibody to an amino acid sequence described in any one of SEQ ID NOs: 7 through 10 or 12.

Thus, the present invention also relates to a recombinant vector containing the above-mentioned DNA, and more particularly, to an expression vector and a host transformed with the vector. Both prokaryotes and eukaryotes can be used for the host. Examples of prokaryotes that can be routinely used for the host include bacteria, for example, the genus Escherichia such as Escherichia coli, and the genus Bacillus such as Bacillus subtilis.

Examples of eukaryotes that can be used include lower eukaryotes such as eucaryotic microorganisms including fungi such as yeast or mold. Examples of yeast includes the genus Saccharomyces such as Saccharomyces cerevisiae, while examples of molds include the genus Aspergillus such as Aspergillus oryzae and Aspergillus niger, as well as the genus Penicillium. Moreover, animal or plant cells can also be used, examples of animal cells including mouse, hamster, monkey and human cell systems. Moreover, insect cells such as silkworm cells or adult silkworms themselves can be used as hosts.

The expression vectors of the present invention contain an expression control region, such as a promoter, terminator or an origin of replication, depending on the type of host in which they are to be introduced. Examples of promoters of bacterial expression vectors include conventionally used promoters such as trc promoter, tac promoter and lac promoter, while examples of yeast promoters include glyceroaldehyde triphosphate dehydrogenase promoter and PH05 promoter. Examples of mold promoters include amylase and trpC. In addition, examples of promoters for animal cell hosts include viral promoters such as SV40 early promoter and SV40 late promoter.

Preparation of expression vector can be performed in accordance with standard methods using restriction enzyme, ligase and so forth. In addition, transformation of a host by an expression vector can also be performed in accordance with standard methods.

In the process for producing the above-mentioned protein, a host transformed with the expression vector is cultured, cultivated or bred, the target protein can be recovered and purified from the resulting culture in accordance with standard methods, examples of which include filtration, centrifugation, cell homogenation, gel filtration chromatography and ion exchange chromatography.

Furthermore, although the present specification

describes transferases derived from Perilla, verbena, torenia and petunia wherein the transferases that transfer glycoside to the 5 position of a flavonoid (which may be simply referred to as "glycosyltransferase" in the present invention), a gene that codes for said enzyme can be cloned, by entirely or partially altering the purification method of said enzyme so as to purify a glycosyltransferase of another plant, and determining the amino acid sequence of said enzyme. Moreover, by using cDNA of the glycosyltransferase derived from Perilla of the present invention as a probe, cDNA of a different glycosyltransferase was able to be obtained from Perilla, and cDNA of a different glycosyltransferase was able to be obtained from a different plant. Thus, other glycosyltransferase genes can be obtained by using a portion or the entirety of a glycosyltransferase gene.

In addition, as indicated in the present specification, by purifying glycosyltransferase from Perilla, verbena, torenia and petunia to obtain antibody to said enzyme in accordance with standard methods, cDNA or chromosomal DNA produces protein which reacts with that antibody that can be cloned. Thus, the present invention is not limited to only genes of glycosyltransferases derived from Perilla, verbena, torenia and petunia, but also relates to glycosyltransferase in the broad sense.

Moreover, the present invention also relates to a plant, its progeny or their tissue for which color has been adjusted by introduction of glycosyltransferase gene, and their form may be that of cut flowers as well.

In addition, UDP-glucose is an example of a glycoside donor in the glycoside transfer reaction of glycoside that include anthocyanin in the present specification.

Examples

The following provides a detailed explanation of the present invention based on Examples. Unless specified otherwise, the experimental procedure was performed in

accordance with the methods described in Molecular Cloning (Cold Spring Harbor, 1989), New Biochemistry Experimental Manual (Kagaku Dojin, 1996) and International Patent Laid-Open Publication No. WO96/25500.

Example 1 Cloning of a Gene Specifically Expressed in Red Forma

(1) Differential Display

Perilla (Perilla frutescens) includes varieties that accumulate anthocyanins in their leaves (for example, red forma (Sakata-no-tane)), and varieties that do not accumulate anthocyanins (for example, blue forma (Sakata-no-tane)). The structure of the major anthocyanin is reported to be malonylshisonin (3-0-(6-0-(p-cumaloyl)-β-D-glucosyl)-5-0-(6-0-malonyl-β-D-glucosyl)-cyanidin) (Agri. Biol. Chem., 53:197-198, 1989).

Differential display is a method reported in Science, 257, 967-971 (1992), and is used, for example, to obtain genes that are expressed tissue-specifically.

Total RNA was extracted from the leaves of the above-mentioned two types of Perilla by the hot phenol method (Plant Molecular Biology Manual, Kluwer Academic Publishers, 1994, pp. D5/1-13). Poly A + RNA was purified from the resulting total RNA using an mRNA separator kit (Clonetech). 0.9 μg of poly A + RNA were reverse-transcribed in 33 μl of reaction mixture using oligo-dT primer added an anchor (GenHunter, H-T11G, H-T11A and H-T11C) to obtain single strand cDNA. Using this cDNA as a template, PCR was performed using the same oligo-dT primer added an anchor and synthetic primers (GenHunter, H-AP1 through 8) as primers.

The volume of the PCR reaction mixture was 20 μl, and it contained 2 μl of cDNA solution, 0.2 μM of any one of H-T11G, H-T11A or H-T11C primer, 0.2 μM of any primer from H-AP1 through H-AP8, 0.12 μM dNTP, 5 or 10 μCi of [^{32}P]dCTP, 10 mM Tris-HCl (pH 9.0), 50 mM KCl, 0.01% Triton X-100, 1.25 mM $MgCl_2$ and 1 unit of Taq polymerase. The reaction conditions comprised holding the temperature at

72°C for 20 seconds followed by repeating the reaction for 40 cycles with one cycle comprising raising the temperature to 94°C for 30 seconds, lowering to 40°C for 2 minutes and raising to 72°C for 30 seconds, and then holding the temperature at 72°C for 5 minutes.

The DNA fragments amplified in this manner were separated by the same polyacrylamide gel electrophoresis as used for DNA Sequencing. After drying the gel, the gel was exposed to X-ray film. Among the resulting approximately 2,600 bands, there were 36 bands observed only in the red forma as a result of comparing the two varieties. They were cut out of the dried gel and eluted into 100 μl of water. The eluted DNA was precipitated with ethanol and dissolved in 20 μl of water. Using a half amount of each DNA as a template, the PCR reaction was performed as described above, and amplified fragments were obtained for 33 of DNA fragments. Library screening and northern analysis were then performed using these DNA fragments.

(2) Northern Analysis

Northern analysis was performed according to the method described below using the above 33 types of DNA probes. After separating poly A + RNA derived from red forma and green forma with formamide gel containing 1.2% agarose, the poly A + RNA was transferred to a Nylon membrane. This membrane was hybridized with the above-mentioned DNA probes labeled with [^{32}P] for overnight at 65°C in the presence of 5XSSPE, 5X Denhalt's solution, 0.5% SDS and 20 μg/ml of denatured salmon sperm DNA. The hybridized membrane was washed at 65°C in 1XSSPE and 0.1% SDS solution and subjected to autoradiography. As a result, only five probes were specifically expressed in red forma. These clones are predicted to be genes involved in the biosynthesis of anthocyanins.

(3) Screening of cDNA Library

A cDNA library with λgt10 as a vector was prepared using the poly A + RNA obtained from the leaves of red

forma and the Complete Rapid Cloning System λgt10 (Amersham). This cDNA library was screened with the five DNA fragments described above to obtain cDNA corresponding to each fragment. Among these, a clone named 3R5 was obtained using a DNA fragment obtained by H-T11A and H-AP3 primers, and this clone demonstrated homology of approximately 26% at the amino acid level with previously reported corn flavonoid-3-0-glucosyl transferase.

In addition, clones designated as 3R4 and 3R6 were obtained by library screening using the same probes, and these demonstrated an extremely high level of homology with 3R5. The complete nucleotide sequences and deduced amino acid sequences of 3R4 and 3R6 are shown in SEQ ID NO: 1 and SEQ ID NO: 2 of the Sequence Listing, respectively. In addition, the deduced amino acid sequences of the proteins encoded by 3R4 and 3R6 demonstrated homology of 92%.

A clone designated as 8R6 was obtained using a DNA fragment obtained by H-T11G and H-AP8 primers, and this clone did not demonstrate significant homology with any sequences reported so far. This sequence is shown in SEQ ID NO: 5 of the Sequence Listing. Although there is a strong possibility that 8R6 is a gene involved in the biosynthesis of anthocyanins, since its structure lacks homology with genes reported so far, it is predicted to be a new gene involved in anthocyanin biosynthesis.

In consideration of the anthocyanin structure in Perilla (the previously mentioned malonylshisonin), it is predicted that this gene is a malonyl transferase. In order to verify this, this gene should be expressed in yeast and E. coli followed by reacting with anthocyanin and malonyl-CoA as substrates. Such an experiment can be carried out using, for example, the method described in International Publication No. WO96/25500. Malonyl transferase gene is useful in terms of artificially altering anthocyanin structure.

(4) Expression of 3R4 cDNA in Yeast

An approximately 1.5 kb DNA fragment obtained by blunting the BstXI cleavaged site of p3R4 using T4 DNA polymerase (Takara Shuzo) and then cutting out at the BamHI cleavage site in the adapter, and an approximately 8 kb DNA fragment obtained by blunting the EcoRI cleaved end of pYE22m and then digesting with BamHI were ligated to obtain a plasmid that was designated as pY3R4.

Furthermore, E. coli strain JM109 having pYE22m was named Escherichia coli SBM335, and deposited at the National Institute of Bioscience and Human-Technology Agency of Industrial Science and Technology as FERM BP-5435. In pY3R4, cDNA coding for glycosyltransferase has been ligated downstream of the promoter for glyceroaldehyde triphosphate dehydrogenase lone of the constitutive yeast promoter, and transcription is controlled by this promoter.

Using pY3R4, yeast Saccharomyces cerevisiae G1315 (Ashikari, et al., Appl. Microbiol. Biotechnol., 30, 515-520, 1989) was transformed according to the method of Ito, et al. (Ito, et al., J. Bacteriol., 153, 163-168, 1983). The transformed yeast was selected according to recovery of tryptophan synthesis ability. The resulting transformed strain was cultured for 24 hours at 30°C with shaking in 10 ml of Burkholder's medium (Burkholder, Amer. J. Bot., 30, 206-210) containing 1% casamino acids.

In order to conduct a control experiment, yeast that spontaneously recovered tryptophan synthesis ability was also cultured in the same manner. After collecting the yeast, the cells were suspended in suspension buffer (100 mM phosphate buffer (pH 8.5), 0.1% (v/v) 2-mercaptoethanol, 10 μM APMSF and 100 μM UDP-glucose) followed by the addition of glass beads (Glass Beads, 425-600 microns Acid-Wash, Sigma) and vigorous shaking to crush the cells. The crushed cells were then centrifuged for 20 minutes at 15,000 rpm and the supernatant was used as a crude enzyme solution for the measurement of enzyme activity described below.

(5) Measurement of Enzymatic Activity

After allowing 50 µl of reaction mixture containing 20 µl of crude enzyme solution (100 mM phosphate buffer (pH 8.5), 670 µM cyanidin-3-glucoside, 1 mM UDP-glucose) for 10 minutes at 30 °C, 50 µl of 50% acetonitrile solution containing 0.1% TFA was added to stop the reaction. Supernatant obtained by centrifuging for 5 minutes at 15,000 rpm was passed through a Samprep LCR4(T)-LC filter (Millipore) so as to remove impurities. This was then analyzed by high-performance liquid chromatography (HPLC). Analysis was performed using a reverse phase column (Asahipak ODP-50, 4.6 mm diameter x 250 mm, Showa Denko), the mobile phase consisted of 0.5% TFA/H_2O for solution A and 0.5% TFA 50% CH_3CN for solution B. The flow rate was 0.6 ml/min. and the fractions were eluted at a gradient of B20% → B100% (20 min) followed by holding at B100% for 5 minutes.

20 µl of reaction mixture was used for analysis. A520 nm, AUFS 0.5 (Shimadzu SPD-10A) and a photodiode array detector (Shimadzu SPD-M6A) at an absorbance of 600-250 nm were used for detection. In the case of reaction of yeast crude enzyme solution that expressed pY3R4, in addition to the substrate cyanidin-3-glucoside (retention time: 17 minutes), a new peak was observed at retention time of 14.5 minutes. Since it was not observed in the case of reaction of yeast crude enzyme solution of the control experiment, this new peak was considered to be generated due to the activity of protein originated from pY3R4. As a result of co-chromatography with cyanidin-3,5-diglucoside, the retention time of this peak coincided with that of cyanidin-3,5-diglucoside, and their absorption spectra were also identical to each other. Based on these observations, 3R4 cDNA of Perilla was found to code for 5GT.

Example 2 Cloning of 5GT Gene of Verbena hybrida

(1) Preparation of cDNA Library

Petals were collected from Verbena variety Hanatemari

violet (Suntory) and ground by a mortar and pestle in liquid nitrogen. RNA was extracted from the ground tissues according to a method using guanidine thiocyanate/cesium chloride, and poly A + RNA was obtained by the method recommended by the manufacturer using Oligotex (Takara Shuzo). The method using guanidine thiocyanate/cesium chloride was carried out in accordance with the method described in detail in Methods in Molecular Biology, Vol. 2 (Humana Press Inc., 1984) by R. McGookin and Robert J. Slater, et al.

Using the resulting poly A + RNA as a template, double-stranded cDNA was synthesized using the ZAP-cDNA synthesis kit (Stratagene), then, a cDNA library was prepared using the Uni-ZAP XR Cloning Kit (Stratagene) according to the method recommended by the manufacturer.

(2) Cloning of 5GT cDNA

The λ phage library obtained as described above was screened in the following manner using the p3R4 cDNA of Perilla as a probe. The filters were maintained at 42°C for 1 hour in hybridization buffer (5X SSC, 30% formamide, 50 mM sodium phosphate buffer (pH 7.0), 3% SDS 2% blocking reagent (Boehringer), 0.1% lauroylsarcosine, 80 μg/ml of salmon sperm DNA). DIG-labeled Perilla 5GT cDNA, p3R4 cDNA, fragment was added to the hybridization solution and the filters were incubated for further 16 hours.

After washing the filters with washing solution (5X SSC 50°C, 1% SDS), the positive clones labeled with anti-DIG-alkaline phosphate were immunologically detected using 5-bromo-4-chloro-3-indolylphosphate and nitro blue tetrazolium salt according to the method described by the manufacturer (Boehringer).

As a result, seven positive clones were obtained. These cDNA were excised on plasmid pBluescript SK using the method recommended by Stratagene. When the lengths of the cDNA were investigated by agarose gel electrophoresis, insertion of a maximum length of 2.0 kb was observed.

(3) Determination of Nucleotide Sequence

Plasmids were extracted from the resulting clones, and the nucleotide sequences near the 3' and 5' ends of the cDNA were determined according to the dideoxy sequence method using fluorescent reagent as recommended by Perkin-Elmer with the ABI 373A sequencer (Perkin-Elmer). As a result, five of the seven clones had mutually same nucleotide sequences although the lengths of the cDNA were different. The entire nucleotide sequence of pSHGT8 was determined. Determination of nucleotide sequences was performed as described above by either using the Kilo-Sequence Deletion Kit (Takara Shuzo) to obtain a series of deleted cDNA clones, or by using an oligoprimer specific for the internal sequence of pSHGT8.

(4) Comparison of the Nucleotide Sequence and the Amino Acid Sequence

The cDNA inserted into pSHGT8 had the length of 2062 bp, and included an open reading frame (ORF) consisting of 1386 bp in length (including a stop codon). This sequence is shown in SEQ ID NO: 3. The amino acid sequence of this ORF had homology of 68% with the amino acid sequence of Perilla 5GT encoded by p3R4, and homology of 64% with that encoded by p3R6. In addition, it also had homology of 22 to 25% with the 3GTs of monocotyledonous and dicotyledoneous plants, and homology of 21% with petunia 3RT.

(5) Expression in Yeast and Measurement of Enzymatic Activity

An approximately 2.0 kb DNA fragment obtained by digesting pSHGT8 with BamHI/XhoI, and an approximately 8 kb DNA fragment obtained by digesting pYE22m with BamHI/SalI were ligated, and the resulting plasmid was designated as pYHGT8. pYHGT8 was expressed in yeast cells in the same manner as Example 1, and the enzymatic activity of the protein encoded by pSHGT8 was measured. As a result, in the reaction mixture containing the crude enzyme solution of yeast transformed with pYHGT8, a product was obtained that coincided with cyanidin-3,5-

diglucoside in both retention time and absorption spectrum. Based on this observation, the pSHGT8 cDNA of Verbena was determined to code for 5GT.

Example 3 Cloning of Trenia 5GT Gene

(1) Preparation of cDNA Library

Petals were collected from torenia variety Summer Wave Blue (Suntory) and ground in a mortar and pestle in liquid nitrogen. RNA was extracted from the ground tissues according to a method using guanidine thiocyanate/cesium chloride, and poly A + RNA was obtained by the method recommended by the manufacturer using Oligotex (Takara Shuzo). The method using guanidine thiocyanate/cesium chloride was carried out in accordance with the method described in detail in Methods in Molecular Biology, Vol. 2 (Humana Press Inc., 1984) by R. McGookin and Robert J. Slater, et al.

Using the resulting poly A + RNA as a template, double-strand cDNA was synthesized using the ZAP-cDNA synthesis kit of Strategene, then, a cDNA library was prepared using the Uni-ZAP XR Cloning Kit (Stratagene) according to the method recommended by the manufacturer.

(2) Cloning of 5GT cDNA

The λ phage library obtained as described above was screened in the same manner as Example 2 using the p3R4 cDNA of Perilla as a probe. As a result, eight positive clones were obtained. After excision of the cDNA on plasmid pBluescript SK, the lengths of the cDNA were investigated by agarose gel electrophoresis, which revealed that a maximum length of insertion was 1.6 kb.

(3) Determination of Nucleotide Sequence

Plasmids were extracted from the resulting clones, and the nucleotide sequences near both 5' and 3' ends were determined in the same manner as Example 2. As a result, six of the eight clones were considered to have mutually same nucleotide sequences although the lengths of the cDNA were different. The entire nucleotide sequence of pSTGT5 cDNA was determined.

(4) Comparison of the Nucleotide Sequence and the Amino Acid Sequence

The cDNA encoded in pSTGT5 was of 1671 bp in length, and included an open reading frame (ORF) consisting of 1437 bp in length (including a stop codon). This sequence is shown in SEQ ID NO: 4. The amino acid sequence of this ORF had homology of 58% with the amino acid sequence of Perilla 5GT encoded by p3R4, and homology of 57% with that encoded by p3R6, and, homology of 57% with that encoded by Verbena pSHGT8. In addition, it also had homology of 19 to 23% with the 3GT of monocotyledonous and dicotyledoneous plants, and homology of 20% with petunia 3RT.

(5) Expression of 5GT gene in Yeast

An approximately 1.6 kb DNA fragment obtained by digesting pSTGT5 with SmaI/KpnI, and an approximately 8 kb DNA fragment obtained by blunting the EcoRI-digested site of pYE22m and then digesting with KpnI were ligated, and the resulting plasmid was designated as pYTGT5. pYTGT5 was expressed in yeast cells in the same manner as Example 1, and the enzymatic activity of the protein encoded by pSTGT5 was measured. As a result, in the reaction mixture containing the crude enzyme solution of yeast transformed with pYTGT5, a product was obtained that coincided with cyanidin-3,5-diglucoside in both retention time and absorption spectrum. Based on this observation, the pSTGT5 cDNA of Torenia was determined to code for 5GT.

Example 4 Cloning of Petunia 5GT Gene

(1) Preparation of cDNA Library

A cDNA library was prepared by RNA extracted from petals of the Petunia variety Old Glory Blue in the manner described in detail by T. Holton, et al. (Plant Journal, 1993 4: 1003-1010)

(2) Cloning of 5GT cDNA

The cDNA library was screened in the same manner as Example 2 using the mixture of 5GT cDNAs of Perilla, torenia and verbena obtained in the manner described above

as probes. As a result, four positive cDNA clones were obtained and excised on plasmid pBluescript SK. The lengths of the cDNA were investigated by agarose gel electrophoresis, cDNA of a maximum length of 2.0 kb was observed.

(3) Determination of the Nucleotide Sequence

Plasmids were extracted from the resulting clones, and the nucleotide sequence near the 5' end was determined in the same manner as Example 2. As a result, two of the four clones, pSPGT1, were appeared to code an amino acid sequence with a high degree of homology with those of 5GT from Perilla, torenia and verbena obtained thus far. Therefore, the entire nucleotide sequence of pSPGT1 was determined.

(4) Comparison of the Nucleotide Sequence and the Amino Acid Sequence

The pSPGT1 cDNA was 2015 bp in length, and included an open reading frame (ORF) consisting of 1407 bp (including a stop codon). This sequence is shown in SEQ ID NO: 6. The amino acid sequence of this ORF had homology of 57% with that of 5GT encoded by p3R4 of Perilla, homology of 54% with that encoded by p3R6, 55% with that encoded by pSHGT8 of verbena, and 51% of that encoded by pTGT5 of torenia. In addition, it also had homology of 20 to 29% with the 3GT of monocotyledonous and dicotyledoneous plants, and homology of 20% with petunia 3RT. Based on this observation, pSPGT1 cDNA obtained from petunia is considered to code for 5GT.

Industrial Applicability

As has been described above, cDNA coding for enzymes that transfer a glycoside to the 5 position of a flavonoid originating in Perilla, verbena, torenia and petunia were cloned and their nucleotide sequences were determined. In addition, the isolated cDNAs were clearly shown to code for 5GT by the enzymatic activity of their protein expressed in yeast. Introducing of these cDNAs into a

suitable plant expression vector and transferring the resulting expression constructs into a plant makes it possible to provide, increase or decrease 5GT activity in the transformed plant, which leads to regulation of flower color. In addition, by using this enzyme, the structure of anthocyans can be altered or more stable anthocyans can be synthesized either in plants or in vitro.

CLAIMS

1. A gene coding for a protein having activity that transfers a glycoside to the 5 position of a flavonoid.

2. A gene as set forth in claim 1 that codes for a protein having an amino acid sequence described in any one of SEQ ID NOs: 7 through 10 or 12 and having activity that transfers a glycoside to the 5 position of a flavonoid, or a protein having an amino acid sequence modified by addition and/or deletion of one or more amino acids and/or substitutions by one or more other amino acids relative to said amino acids and maintains activity that transfers a glycoside to the 5 position of a flavonoid.

3. A gene as set forth in claim 1 that codes for a protein having an amino acid sequence that has homology of 30% or more with an amino acid sequence described in any one of SEQ ID NOs: 7 through 10 or 12, and has activity that transfers a glycoside to the 5 position of a flavonoid.

4. A gene as set forth in claim 1 that codes for a protein having an amino acid sequence that has homology of 50% or more with an amino acid sequence described in any one of SEQ ID NOs: 7 through 10 or 12, and has activity that transfers a glycoside to the 5 position of a flavonoid.

5. A gene as set forth in claim 1 that codes for a protein, wherein said gene can be hybridized under conditions of 5 x SCC and 50°C with all or a portion of a nucleotide sequence that codes for an amino acid sequence described in any one of SEQ ID NOs: 7 through 10 or 12, and has activity that transfers a glycoside to the 5 position of a flavonoid.

6. A vector containing a gene as set forth in any one of claims 1 through 5.

7. A host transformed with a vector as set forth in claim 6.

8. A protein encoded by a gene as set forth in any one of claims 1 through 5.

9. A process for producing a protein comprising culturing or breeding a host as set forth in claim 7, and recovering a protein having activity that transfers a glycoside to the 5 position of a flavonoid from said host.

10. A plant into which is introduced a gene as set forth in any one of claims 1 through 5, or its progeny or tissue having identical properties.

11. A cut flower of the plant as set forth in claim 10 or its progeny having identical properties.

ABSTRACT

The present invention provides a gene that codes for a protein having an amino acid sequence described in any of SEQ ID NOs: 7 through 10 or 12 and having activity that transfers a glycoside to the 5 position of a flavonoid, a gene that codes for a protein having a modified amino acid sequence relative to the above amino acid sequence and having activity that transfers a glycoside to the 5 position of a flavonoid, and a process for producing the above protein using said gene. This gene can be used to artificially alter the color of plants.

SEQUENCE LISTING

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Lys Leu Val Arg Glu Asn Ala Ile Lys Trp Lys Thr Leu Ala Arg Gln
425 430 435 440
gcc atg gga taggatggat cttcactcaa caatctcaac gcctttcttc 1393
Ala Met Gly
443
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taaaaaaaaa aaaaaaa 1470

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Met Ser Arg Ala His Val Leu Leu Ala
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Thr Phe Pro Ala Gln Gly His Ile Asn Pro Ala Leu Gln Phe Ala Lys
10 15 20 25
cgt ctc gca aat gcc gac att caa gtc aca ttc ttc acc agc gtc tac 148
Arg Leu Ala Asn Ala Asp Ile Gln Val Thr Phe Phe Thr Ser Val Tyr
30 35 40
gca tgg cgc cgc atg tcc aga acc gcc gct ggc tca aac ggg ctc atc 196
Ala Trp Arg Arg Met Ser Arg Thr Ala Ala Gly Ser Asn Gly Leu Ile
45 50 55
aat ttt gtg tcg ttt tcc gac ggg tat gac gac ggg tta cag ccc gga 244
Asn Phe Val Ser Phe Ser Asp Gly Tyr Asp Asp Gly Leu Gln Pro Gly
60 65 70

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gac gat ggg aag aac tac atg tcg gag atg aaa agc aga ggt ata aaa      292
Asp Asp Gly Lys Asn Tyr Met Ser Glu Met Lys Ser Arg Gly Ile Lys
     75                  80                  85
gcc ttg agc gat act ctt gca gcc aat aat gtc gat caa aaa agc agc      340
Ala Leu Ser Asp Thr Leu Ala Ala Asn Asn Val Asp Gln Lys Ser Ser
90                  95                 100                 105
aaa atc acg ttc gtg gtg tac tcc cac ctc ttt gca tgg gcg gcc aag      388
Lys Ile Thr Phe Val Val Tyr Ser His Leu Phe Ala Trp Ala Ala Lys
                110                 115                 120
gtg gcg cgt gag ttc cat ctc cgg agc gcg cta ctc tgg att gag cca      436
Val Ala Arg Glu Phe His Leu Arg Ser Ala Leu Leu Trp Ile Glu Pro
            125                 130                 135
gct acg gtg ttg gat ata ttt tac ttt tat ttc aac ggc tat agc gac      484
Ala Thr Val Leu Asp Ile Phe Tyr Phe Tyr Phe Asn Gly Tyr Ser Asp
        140                 145                 150
gaa atc gat gcg ggt tcg gat gct att cac ttg ccc gga gga ctc cca      532
Glu Ile Asp Ala Gly Ser Asp Ala Ile His Leu Pro Gly Gly Leu Pro
    155                 160                 165
gtg ctg gcc cag cgt gat tta ccg tct ttc ctt ctt cct tcc acg cat      580
Val Leu Ala Gln Arg Asp Leu Pro Ser Phe Leu Leu Pro Ser Thr His
170                 175                 180                 185
gag aga ttc cgt tca ctg atg aag gag aaa ttg gaa act tta gaa ggt      628
Glu Arg Phe Arg Ser Leu Met Lys Glu Lys Leu Glu Thr Leu Glu Gly
                190                 195                 200
gaa gaa aaa cct aag gtc ttg gtg aac agc ttt gat gcg ttg gag cct      676
Glu Glu Lys Pro Lys Val Leu Val Asn Ser Phe Asp Ala Leu Glu Pro
            205                 210                 215
gat gcg ctc aag gcc att gat aag tac gag atg att gca atc ggg ccg      724
Asp Ala Leu Lys Ala Ile Asp Lys Tyr Glu Met Ile Ala Ile Gly Pro
        220                 225                 230
ttg att cct tcc gca ttc ttg gac ggt aaa gat cct tcg gac agg tct      772
Leu Ile Pro Ser Ala Phe Leu Asp Gly Lys Asp Pro Ser Asp Arg Ser
    235                 240                 245
ttc ggc gga gat ttg ttc gag aaa ggg tcg aat gac gac gat tgc ctc      820
Phe Gly Gly Asp Leu Phe Glu Lys Gly Ser Asn Asp Asp Asp Cys Leu
250                 255                 260                 265
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gaa tgg ttg agc acg aat cct cga tct tcg gtg gtt tac gtt tcg ttc      868
Glu Trp Leu Ser Thr Asn Pro Arg Ser Ser Val Val Tyr Val Ser Phe
                270                 275                 280
gga agc ttc gtt aat acg acg aag tcg caa atg gaa gag ata gca aga      916
Gly Ser Phe Val Asn Thr Thr Lys Ser Gln Met Glu Glu Ile Ala Arg
            285                 290                 295
ggg ctg tta gat tgt ggg agg ccg ttt ttg tgg gtg gta aga gta aac      964
Gly Leu Leu Asp Cys Gly Arg Pro Phe Leu Trp Val Val Arg Val Asn
        300                 305                 310
gaa gga gaa gag gta ttg ata agt tgc atg gag gag ttg aaa cga gtg     1012
Glu Gly Glu Glu Val Leu Ile Ser Cys Met Glu Glu Leu Lys Arg Val
    315                 320                 325
ggg aaa att gta tct tgg tgt tct caa ttg gaa gtc ctg acg cat ccc     1060
Gly Lys Ile Val Ser Trp Cys Ser Gln Leu Glu Val Leu Thr His Pro
330                 335                 340                 345
tcg ttg gga tgt ttc gtg aca cac tgc ggg tgg aat tcg act cta gag     1108
Ser Leu Gly Cys Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu Glu
                350                 355                 360
agt ata tct ttc ggg gtt ccg atg gtg gct ttt ccg cag tgg ttc gat     1156
Ser Ile Ser Phe Gly Val Pro Met Val Ala Phe Pro Gln Trp Phe Asp
            365                 370                 375
caa ggg acg aat gcg aag ctg atg gag gat gtg tgg agg acg ggt gtg     1204
Gln Gly Thr Asn Ala Lys Leu Met Glu Asp Val Trp Arg Thr Gly Val
        380                 385                 390
aga gtg aga gct aat gag gag ggt agc gtc gtt gat ggt gat gaa att     1252
Arg Val Arg Ala Asn Glu Glu Gly Ser Val Val Asp Gly Asp Glu Ile
    395                 400                 405
agg aga tgt att gag gag gtt atg gat ggg gga gaa aag agt agg aaa     1300
Arg Arg Cys Ile Glu Glu Val Met Asp Gly Gly Glu Lys Ser Arg Lys
410                 415                 420                 425
ctt aga gag agt gct ggc aag tgg aag gat ttg gca aga aaa gct atg     1348
Leu Arg Glu Ser Ala Gly Lys Trp Lys Asp Leu Ala Arg Lys Ala Met
                430                 435                 440
gag gaa gat gga tct tca gtt aac aac ctc aag gtc ttt ctt gat gag     1396
Glu Glu Asp Gly Ser Ser Val Asn Asn Leu Lys Val Phe Leu Asp Glu
            445                 450                 455
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gtt gta ggt atc taaagacgta aatgaggtcc ccataggcaa aattgcaaat 1448
Val Val Gly Ile
460 461

ttcatctcgt aagttgaata ctttttggct ttaattttgt tcgagtttgt ttttcaaaat 1508
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gactaacttt gtacaaaatg aaaagttata tgatgaaatt ttaaaaaaca aactcagaca 1868
ataataaagc ccgaaagtag taaaattacc tgacgaaatt tgcaatttcg cctcctattt 1928
taatttttt ggtgtgttta ataaatcggt tattttactt ttaattaaaa taaaagtgag 1988
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Met Val Asn
1

aaa cgc cat att cta cta gca aca ttc cca gca caa ggc cac ata aac 101
Lys Arg His Ile Leu Leu Ala Thr Phe Pro Ala Gln Gly His Ile Asn
5 10 15

cct tct ctc gag ttc gcc aaa agg ctc ctc aac acc gga tac gtc gac 149
Pro Ser Leu Glu Phe Ala Lys Arg Leu Leu Asn Thr Gly Tyr Val Asp
20 25 30 35

caa gtc aca ttc ttc acg agt gta tac gca ttg aga cgc atg cgc ttc 197
Gln Val Thr Phe Phe Thr Ser Val Tyr Ala Leu Arg Arg Met Arg Phe
40 45 50

gaa acc gat ccg agc agc aga atc gat ttc gtg gca tkt yca gat tct 245
Glu Thr Asp Pro Ser Ser Arg Ile Asp Phe Val Ala Xaa Xaa Asp Ser
55 60 65

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tac gat gat ggc tta aag aaa ggc gac gat ggc aaa aac tac atg tcg      293
Tyr Asp Asp Gly Leu Lys Lys Gly Asp Asp Gly Lys Asn Tyr Met Ser
          70                  75                  80
gag atg aga aag cgc gga acg aag gcc tta aag gac act ctt att aag      341
Glu Met Arg Lys Arg Gly Thr Lys Ala Leu Lys Asp Thr Leu Ile Lys
     85                  90                  95
ctc aac gat gct gcg atg gga agt gaa tgt tac aat cgc gtg agc ttt      389
Leu Asn Asp Ala Ala Met Gly Ser Glu Cys Tyr Asn Arg Val Ser Phe
100                 105                 110                 115
gtg gtg tac tct cat cta ttt tcg tgg gca gct gaa gtg gcg cgt gaa      437
Val Val Tyr Ser His Leu Phe Ser Trp Ala Ala Glu Val Ala Arg Glu
                120                 125                 130
gtc gac gtg ccg agt gcc ctt ctt tgg att gaa ccg gct acg gtt ttc      485
Val Asp Val Pro Ser Ala Leu Leu Trp Ile Glu Pro Ala Thr Val Phe
            135                 140                 145
gat gtg tac tat ttt tac ttc aat ggg tat gcc gat gat atc gat gcg      533
Asp Val Tyr Tyr Phe Tyr Phe Asn Gly Tyr Ala Asp Asp Ile Asp Ala
        150                 155                 160
ggc tca gat caa atc caa ctg ccc aat ctt ccg cag ctc tcc aag caa      581
Gly Ser Asp Gln Ile Gln Leu Pro Asn Leu Pro Gln Leu Ser Lys Gln
    165                 170                 175
gat ctc ccc tct ttc cta ctc cct tcg agc ccc gcg aga ttc cga acc      629
Asp Leu Pro Ser Phe Leu Leu Pro Ser Ser Pro Ala Arg Phe Arg Thr
180                 185                 190                 195
cta atg aaa gaa aag ttc gac acg ctc gac aaa gaa ccg aaa gcg aag      677
Leu Met Lys Glu Lys Phe Asp Thr Leu Asp Lys Glu Pro Lys Ala Lys
                200                 205                 210
gtc ttg ata aac acg ttc gac gca tta gaa acc gaa caa ctc aaa gcc      725
Val Leu Ile Asn Thr Phe Asp Ala Leu Glu Thr Glu Gln Leu Lys Ala
            215                 220                 225
atc gac agg tat gaa cta ata tcc atc ggc cca tta atc cca tca tcg      773
Ile Asp Arg Tyr Glu Leu Ile Ser Ile Gly Pro Leu Ile Pro Ser Ser
        230                 235                 240
ata ttc tca gat ggc aac gac ccc tca tca agc aac aaa tcc tac ggt      821
Ile Phe Ser Asp Gly Asn Asp Pro Ser Ser Ser Asn Lys Ser Tyr Gly
    245                 250                 255
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gga gac ctc ttc aga aaa gcc gat gaa act tac atg gac tgg cta aac      869
Gly Asp Leu Phe Arg Lys Ala Asp Glu Thr Tyr Met Asp Trp Leu Asn
260                 265                 270                 275
tca aaa ccc gaa tca tcg gtc gtt tac gtt tcg ttc ggg agc ctc ctg      917
Ser Lys Pro Glu Ser Ser Val Val Tyr Val Ser Phe Gly Ser Leu Leu
                280                 285                 290
agg ctc ccg aaa ccc caa atg gaa gaa ata gca ata ggg ctt tca gac      965
Arg Leu Pro Lys Pro Gln Met Glu Glu Ile Ala Ile Gly Leu Ser Asp
            295                 300                 305
acc aaa tcg cca gtt ctc tgg gtg ata aga aga aac gaa gag ggc gac     1013
Thr Lys Ser Pro Val Leu Trp Val Ile Arg Arg Asn Glu Glu Gly Asp
        310                 315                 320
gaa caa gag caa gca gaa gaa gaa gag aag ctg ctg agc ttc ttt gat     1061
Glu Gln Glu Gln Ala Glu Glu Glu Glu Lys Leu Leu Ser Phe Phe Asp
    325                 330                 335
cgt cac gga act gaa cga ctc ggg aaa atc gtg aca tgg tgc tca caa     1109
Arg His Gly Thr Glu Arg Leu Gly Lys Ile Val Thr Trp Cys Ser Gln
340                 345                 350                 355
ttg gat gtt ctg acg cat aag tcg gtg gga tgc ttc gtg acg cat tgc     1157
Leu Asp Val Leu Thr His Lys Ser Val Gly Cys Phe Val Thr His Cys
                360                 365                 370
ggt tgg aat tct gct atc gag agc ctg gct tgt ggt gtg ccc gtg gtg     1205
Gly Trp Asn Ser Ala Ile Glu Ser Leu Ala Cys Gly Val Pro Val Val
            375                 380                 385
tgc ttt cct caa tgg ttc gat caa ggg act aat gcg aag atg atc gaa     1253
Cys Phe Pro Gln Trp Phe Asp Gln Gly Thr Asn Ala Lys Met Ile Glu
        390                 395                 400
gat gtg tgg agg agt ggt gtg aga gtc aga gtg aat gag gaa ggc ggc     1301
Asp Val Trp Arg Ser Gly Val Arg Val Arg Val Asn Glu Glu Gly Gly
    405                 410                 415
gtt gtt gat agg cgt gag att aag agg tgc gtc tcg gag gtt ata aag     1349
Val Val Asp Arg Arg Glu Ile Lys Arg Cys Val Ser Glu Val Ile Lys
420                 425                 430                 435
agt cga gag ttg aga gaa agc gca atg atg tgg aag ggt ttg gct aaa     1397
Ser Arg Glu Leu Arg Glu Ser Ala Met Met Trp Lys Gly Leu Ala Lys
                440                 445                 450
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gaa gct atg gat gaa gaa cgt gga tca tca atg aac aat ctg aag aat 1445
Glu Ala Met Asp Glu Glu Arg Gly Ser Ser Met Asn Asn Leu Lys Asn
455 460 465

ttt att act agg att att aat gaa aat gcc tca taagttgtac 1488
Phe Ile Thr Arg Ile Ile Asn Glu Asn Ala Ser
470 475 478

tatatatgtt attattgttg ttatggacgt cgaattaagt attagttaaa tgatatgtat 1548

ttagaggaag gccaaaacgg gctacacccg gcaggccacg ggttggaaaa gcccgccatg 1608

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aaa 1671

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agtgggtttt gttactcagc ttcaacctac gtacgtacta ctactgactc aactctcaag 180

agaatgaata taatatataa tgggcgatag atctttgtag atatgtaggt gtagcctgca 240

ggtggttaat taatttccgg tgtgggaaaa taaataaata aataaatata gcg atg agc 299
Met Ser
1

agc agc agc agc aga agg tgg aga gag aat gag ggg atg cga agg aca 347
Ser Ser Ser Ser Arg Arg Trp Arg Glu Asn Glu Gly Met Arg Arg Thr
5 10 15

ttg ctg ggg ttg ggt ttg ggg cag ttg gtt tct ttc gat ttg gct atc 395
Leu Leu Gly Leu Gly Leu Gly Gln Leu Val Ser Phe Asp Leu Ala Ile
20 25 30

atg acc ttt tct gct tct ttg gtt tca acc aca gtg gat gca cca ctt 443
Met Thr Phe Ser Ala Ser Leu Val Ser Thr Thr Val Asp Ala Pro Leu
35 40 45 50

act atg tcg ttc act aca tac act gtt gtg gcc ctg ctc tat gga acc 491
Thr Met Ser Phe Thr Thr Tyr Thr Val Val Ala Leu Leu Tyr Gly Thr
55 60 65

atc ttg ctt tac cgc cgc cac aaa ttc ttg gtt cca tgg tac tgg tat 539
Ile Leu Leu Tyr Arg Arg His Lys Phe Leu Val Pro Trp Tyr Trp Tyr
70 75 80

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gct ctc ctg ggg ttc gtg gac gtc cac ggc aat tat ctt gtt aat aaa      587
Ala Leu Leu Gly Phe Val Asp Val His Gly Asn Tyr Leu Val Asn Lys
         85                  90                  95
gca ttc gag ttg aca tcg att acg agt gtg agc ata ctg gat tgt tgg      635
Ala Phe Glu Leu Thr Ser Ile Thr Ser Val Ser Ile Leu Asp Cys Trp
    100                 105                 110
aca atc gtg tgg tcc atc atc ttt aca tgg atg ttc cta ggc aca aaa      683
Thr Ile Val Trp Ser Ile Ile Phe Thr Trp Met Phe Leu Gly Thr Lys
115                 120                 125                 130
tac tct gta tac cag ttt gtc ggt gct gct att tgt gta gga ggc ctc      731
Tyr Ser Val Tyr Gln Phe Val Gly Ala Ala Ile Cys Val Gly Gly Leu
                135                 140                 145
ctc ctc gtg ctt ctt tcc gac tca ggg gtc act gct gct ggt tcg aat      779
Leu Leu Val Leu Leu Ser Asp Ser Gly Val Thr Ala Ala Gly Ser Asn
            150                 155                 160
cct ctt ttg ggt gat ttt ctt gtc ata aca ggc tct att ttg ttc aca      827
Pro Leu Leu Gly Asp Phe Leu Val Ile Thr Gly Ser Ile Leu Phe Thr
        165                 170                 175
ctc agc act gtt ggt cag gaa tac tgc gtg aag agg aaa gat cgt att      875
Leu Ser Thr Val Gly Gln Glu Tyr Cys Val Lys Arg Lys Asp Arg Ile
    180                 185                 190
gaa gta gta gca atg atc ggt gta ttt ggt atg ctc atc agt gca acc      923
Glu Val Val Ala Met Ile Gly Val Phe Gly Met Leu Ile Ser Ala Thr
195                 200                 205                 210
gag att act gtg ctg gag agg aat gcc ctc tca tca atg cag tgg tct      971
Glu Ile Thr Val Leu Glu Arg Asn Ala Leu Ser Ser Met Gln Trp Ser
                215                 220                 225
act gga ctt ttg gca gcc tat gtt gtt tat gca ctg tcc agc ttc ctc     1019
Thr Gly Leu Leu Ala Ala Tyr Val Val Tyr Ala Leu Ser Ser Phe Leu
            230                 235                 240
ttc tgc aca ctc acc cct ttt ctt ctc aag atg agt ggc gct gca ttt     1067
Phe Cys Thr Leu Thr Pro Phe Leu Leu Lys Met Ser Gly Ala Ala Phe
        245                 250                 255
ttc aat ctt tcc atg ctt aca tct gat atg tgg gct gtt gca att agg     1115
Phe Asn Leu Ser Met Leu Thr Ser Asp Met Trp Ala Val Ala Ile Arg
    260                 265                 270
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aca ttc ata tac aac cag gag gtt gat tgg tta tac tat ttg gcc ttt 1163
Thr Phe Ile Tyr Asn Gln Glu Val Asp Trp Leu Tyr Tyr Leu Ala Phe
275 280 285 290
tgt ctc gtt gtt gtt gga ata ttc ata tat aca aaa aca gag aag gat 1211
Cys Leu Val Val Val Gly Ile Phe Ile Tyr Thr Lys Thr Glu Lys Asp
295 300 305
cct aac aat acg aga gcc ctt gag aat gga aac ttg gat cat gaa tat 1259
Pro Asn Asn Thr Arg Ala Leu Glu Asn Gly Asn Leu Asp His Glu Tyr
310 315 320
agt ctc ctt gag gat caa gat gac aca cca aga aaa cca tagctagctt 1308
Ser Leu Leu Glu Asp Gln Asp Asp Thr Pro Arg Lys Pro
325 330 335
tgcccacaat cttttcatca acagttttaa ataattcgtg agggggagag agatcgagat 1368
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aacagctatg accatgatta cgccaagctc gaaattaacc ctcactaaag ggaacaaaag 180
ctggagctcc acgcggtggc ggccgctcta gaactagtgg atcccccggg ctgcaggaat 240
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aaaacataca agtttttaat ttttcactaa gcaagaaaat atg gtg cag cct cat gtc 358
Met Val Gln Pro His Val
1 5
atc tta aca aca ttt cca gca caa ggc cat att aat cca gca ctt caa 406
Ile Leu Thr Thr Phe Pro Ala Gln Gly His Ile Asn Pro Ala Leu Gln
10 15 20
ttt gcc aag aat ctt gtc aag atg ggc ata gaa gtg aca ttt tct aca 454
Phe Ala Lys Asn Leu Val Lys Met Gly Ile Glu Val Thr Phe Ser Thr
25 30 35
agc att tat gcc caa agc cgt atg gat gaa aaa tcc att ctt aat gca 502
Ser Ile Tyr Ala Gln Ser Arg Met Asp Glu Lys Ser Ile Leu Asn Ala
40 45 50

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cca aaa gga ttg aat ttc att cca ttt tcc gat ggc ttt gat gaa ggt      550
Pro Lys Gly Leu Asn Phe Ile Pro Phe Ser Asp Gly Phe Asp Glu Gly
55                  60                  65                  70
ttt gat cat tca aaa gac cct gta ttt tac atg tca caa ctt cgt aaa      598
Phe Asp His Ser Lys Asp Pro Val Phe Tyr Met Ser Gln Leu Arg Lys
                75                  80                  85
tgt gga agt gaa act gtc aaa aaa ata att ctc act tgc tct gaa aat      646
Cys Gly Ser Glu Thr Val Lys Lys Ile Ile Leu Thr Cys Ser Glu Asn
            90                  95                  100
gga cag cct ata act tgc cta ctt tac tcc att ttc ctt cct tgg gca      694
Gly Gln Pro Ile Thr Cys Leu Leu Tyr Ser Ile Phe Leu Pro Trp Ala
        105                 110                 115
gca gag gta gca cgt gaa gtt cac atc cct tct gct ctt ctt tgg agt      742
Ala Glu Val Ala Arg Glu Val His Ile Pro Ser Ala Leu Leu Trp Ser
    120                 125                 130
caa cca gca aca ata ttg gac ata tat tac ttc aac ttt cat gga tat      790
Gln Pro Ala Thr Ile Leu Asp Ile Tyr Tyr Phe Asn Phe His Gly Tyr
135                 140                 145                 150
gaa aaa gct atg gct aat gaa tcc aat gat cca aat tgg tcc att caa      838
Glu Lys Ala Met Ala Asn Glu Ser Asn Asp Pro Asn Trp Ser Ile Gln
                155                 160                 165
ctt ccc ggg ctt cca cta ctg gaa act cga gat ctt cct tca ttt tta      886
Leu Pro Gly Leu Pro Leu Leu Glu Thr Arg Asp Leu Pro Ser Phe Leu
            170                 175                 180
ctt cct tat ggt gca aaa ggg agt ctt cga gtt gca ctt cca cca ttc      934
Leu Pro Tyr Gly Ala Lys Gly Ser Leu Arg Val Ala Leu Pro Pro Phe
        185                 190                 195
aaa gaa ttg ata gac aca tta gat gct gaa acc act cct aag att ctt      982
Lys Glu Leu Ile Asp Thr Leu Asp Ala Glu Thr Thr Pro Lys Ile Leu
    200                 205                 210
gtg aat aca ttt gat gaa tta gag cct gag gca ctc aat gca att gaa     1030
Val Asn Thr Phe Asp Glu Leu Glu Pro Glu Ala Leu Asn Ala Ile Glu
215                 220                 225                 230
ggt tat aag ttt tat gga att gga ccg ttg att cct tct gct ttc ttg     1078
Gly Tyr Lys Phe Tyr Gly Ile Gly Pro Leu Ile Pro Ser Ala Phe Leu
                235                 240                 245
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ggt gga aat gac cct tta gat gct tca ttt ggt ggt gat ctt ttt caa    1126
Gly Gly Asn Asp Pro Leu Asp Ala Ser Phe Gly Gly Asp Leu Phe Gln
            250                 255                 260
aat tca aat gac tat atg gaa tgg tta aac tca aag cca aat tca tca    1174
Asn Ser Asn Asp Tyr Met Glu Trp Leu Asn Ser Lys Pro Asn Ser Ser
        265                 270                 275
gtt gtt tat ata tct ttt ggg agt cta atg aat cca tct att agc caa    1222
Val Val Tyr Ile Ser Phe Gly Ser Leu Met Asn Pro Ser Ile Ser Gln
    280                 285                 290
atg gag gag ata tca aaa ggg ttg ata gac ata gga agg ccg ttt tta    1270
Met Glu Glu Ile Ser Lys Gly Leu Ile Asp Ile Gly Arg Pro Phe Leu
295                 300                 305                 310
tgg gtg ata aaa gaa aat gaa aaa ggc aaa gaa gaa gag aat aaa aag    1318
Trp Val Ile Lys Glu Asn Glu Lys Gly Lys Glu Glu Glu Asn Lys Lys
                315                 320                 325
ctt ggt tgt att gaa gaa ttg gaa aaa ata gga aaa ata gtt cca tgg    1366
Leu Gly Cys Ile Glu Glu Leu Glu Lys Ile Gly Lys Ile Val Pro Trp
            330                 335                 340
tgt tca caa ctt gaa gtt cta aaa cat cca tct tta gga tgt ttt gtt    1414
Cys Ser Gln Leu Glu Val Leu Lys His Pro Ser Leu Gly Cys Phe Val
        345                 350                 355
tct cat tgt gga tgg aat tca gcc tta gag agt tta gct tgt gga gtg    1462
Ser His Cys Gly Trp Asn Ser Ala Leu Glu Ser Leu Ala Cys Gly Val
    360                 365                 370
cca gtt gtg gca ttt cct caa tgg aca gat caa atg aca aat gcc aaa    1510
Pro Val Val Ala Phe Pro Gln Trp Thr Asp Gln Met Thr Asn Ala Lys
375                 380                 385                 390
caa gtt gaa gat gtg tgg aaa agt gga gta aga gtg aga ata aat gaa    1558
Gln Val Glu Asp Val Trp Lys Ser Gly Val Arg Val Arg Ile Asn Glu
                395                 400                 405
gat ggt gtt gtt gaa agt gag gaa atc aaa agg tgt att gaa ttg gta    1606
Asp Gly Val Val Glu Ser Glu Glu Ile Lys Arg Cys Ile Glu Leu Val
            410                 415                 420
atg gat gga gga gag aaa ggg gaa gaa ttg aga aag aat gct aag aaa    1654
Met Asp Gly Gly Glu Lys Gly Glu Glu Leu Arg Lys Asn Ala Lys Lys
        425                 430                 435
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tgg aaa gaa ttg gct aga gaa gct gtg aag gaa ggt gga tct tca cac    1702
Trp Lys Glu Leu Ala Arg Glu Ala Val Lys Glu Gly Gly Ser Ser His
    440                 445                 450
aag aat tta aag gct ttt att gat gat gtt gcc aaa ggg ttt taatatttac 1754
Lys Asn Leu Lys Ala Phe Ile Asp Asp Val Ala Lys Gly Phe
455                 460                 465         468
aggcttttgc cgtgatatta cttcccctag ttggcgattc actctttgtg gacttgcttg  1814
acaaaaaact gagggaatgt gctaagacac gctaatgctt taagaagtca tttccaaggc  1874
ttgaagcctg cttttaaaac ttattagcca gtaatctata gggttctctt ctatttttct  1934
ctgtctctct ttttagcctt tttctttcca aggtttaaga atagcgtgaa catagcttag  1994
tacgtagtct tggtatctct atcttaccaa gtgcaagatt atgcttatgc tgtcctccta  2054
aatttcttaa taaaatgcaa gatgaaaaag tacaaaaaaa aaaaaaaaaa a           2105
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<210> 7

<211> 460

<212> PRT

<213> Perilla frutescens

<400> 7

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Met Val Arg Arg Arg Val Leu Leu Ala Thr Phe Pro Ala Gln Gly His
 1               5                  10                  15
Ile Asn Pro Ala Leu Gln Phe Ala Lys Arg Leu Leu Lys Ala Gly Thr
            20                  25                  30
Asp Val Thr Phe Phe Thr Ser Val Tyr Ala Trp Arg Arg Met Ala Asn
        35                  40                  45
Thr Ala Ser Ala Ala Ala Gly Asn Pro Pro Gly Leu Asp Phe Val Ala
    50                  55                  60
Phe Ser Asp Gly Tyr Asp Asp Gly Leu Lys Pro Cys Gly Asp Gly Lys
65                  70                  75                  80
Arg Tyr Met Ser Glu Met Lys Ala Arg Gly Ser Glu Ala Leu Arg Asn
                85                  90                  95
Leu Leu Leu Asn Asn His Asp Val Thr Phe Val Val Tyr Ser His Leu
            100                 105                 110
Phe Ala Trp Ala Ala Glu Val Ala Arg Glu Ser Gln Val Pro Ser Ala
        115                 120                 125
Leu Leu Trp Val Glu Pro Ala Thr Val Leu Cys Ile Tyr Tyr Phe Tyr
    130                 135                 140
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Phe Asn Gly Tyr Ala Asp Glu Ile Asp Ala Gly Ser Asp Glu Ile Gln
145 150 155 160
Leu Pro Arg Leu Pro Pro Leu Glu Gln Arg Ser Leu Pro Thr Phe Leu
165 170 175
Leu Pro Glu Thr Pro Glu Arg Phe Arg Leu Met Met Lys Glu Lys Leu
180 185 190
Glu Thr Leu Asp Gly Glu Glu Lys Ala Lys Val Leu Val Asn Thr Phe
195 200 205
Asp Ala Leu Glu Pro Asp Ala Leu Thr Ala Ile Asp Arg Tyr Glu Leu
210 215 220
Ile Gly Ile Gly Pro Leu Ile Pro Ser Ala Phe Leu Asp Gly Gly Asp
225 230 235 240
Pro Ser Glu Thr Ser Tyr Gly Gly Asp Leu Phe Glu Lys Ser Glu Glu
245 250 255
Asn Asn Cys Val Glu Trp Leu Asp Thr Lys Pro Lys Ser Ser Val Val
260 265 270
Tyr Val Ser Phe Gly Ser Val Leu Arg Phe Pro Lys Ala Gln Met Glu
275 280 285
Glu Ile Gly Lys Gly Leu Leu Ala Cys Gly Arg Pro Phe Leu Trp Met
290 295 300
Ile Arg Glu Gln Lys Asn Asp Asp Gly Glu Glu Glu Glu Glu Glu Leu
305 310 315 320
Ser Cys Ile Gly Glu Leu Lys Lys Met Gly Lys Ile Val Ser Trp Cys
325 330 335
Ser Gln Leu Glu Val Leu Ala His Pro Ala Leu Gly Cys Phe Val Thr
340 345 350
His Cys Gly Trp Asn Ser Ala Val Glu Ser Leu Ser Cys Gly Val Pro
355 360 365
Val Val Ala Val Pro Gln Trp Phe Asp Gln Thr Thr Asn Ala Lys Leu
370 375 380
Ile Glu Asp Ala Trp Gly Thr Gly Val Arg Val Arg Met Asn Glu Gly
385 390 395 400
Gly Gly Val Asp Gly Ser Glu Ile Glu Arg Cys Val Glu Met Val Met
405 410 415

Asp Gly Gly Glu Lys Ser Lys Leu Val Arg Glu Asn Ala Ile Lys Trp
420 425 430
Lys Thr Leu Ala Arg Glu Ala Met Gly Glu Asp Gly Ser Ser Leu Lys
435 440 445
Asn Leu Asn Ala Phe Leu His Gln Val Ala Arg Ala
450 455 460

<210> 8
<211> 443
<212> PRT
<213> Perilla frutescens
<400> 8

Met Val Arg Arg Arg Val Leu Leu Ala Thr Phe Pro Ala Gln Gly His
1 5 10 15
Ile Asn Pro Ala Leu Gln Phe Ala Lys Arg Leu Leu Lys Ala Gly Thr
20 25 30
Asp Val Thr Phe Phe Thr Ser Val Tyr Ala Trp Arg Arg Met Ala Asn
35 40 45
Thr Ala Ser Ala Ala Ala Gly Asn Pro Pro Gly Leu Asp Phe Val Ala
50 55 60
Phe Ser Asp Gly Tyr Asp Asp Gly Leu Lys Pro Gly Gly Asp Gly Lys
65 70 75 80
Arg Tyr Met Ser Glu Met Lys Ala Arg Gly Ser Glu Ala Leu Arg Asn
85 90 95
Leu Leu Leu Asn Asn Asp Asp Val Thr Phe Val Val Tyr Ser His Leu
100 105 110
Phe Ala Trp Ala Ala Glu Val Ala Arg Leu Ser His Val Pro Thr Ala
115 120 125
Leu Leu Trp Val Glu Pro Ala Thr Val Leu Cys Ile Tyr His Phe Tyr
130 135 140
Phe Asn Gly Tyr Ala Asp Glu Ile Asp Ala Gly Ser Asn Glu Ile Gln
145 150 155 160
Leu Pro Arg Leu Pro Ser Leu Glu Gln Arg Ser Leu Pro Thr Phe Leu
165 170 175
Leu Pro Ala Thr Pro Glu Arg Phe Arg Leu Met Met Lys Glu Lys Leu
180 185 190

Glu Thr Leu Asp Gly Glu Glu Lys Ala Lys Val Leu Val Asn Thr Phe
195 200 205
Asp Ala Leu Glu Pro Asp Ala Leu Thr Ala Ile Asp Arg Tyr Glu Leu
210 215 220
Ile Gly Ile Gly Pro Leu Ile Pro Ser Ala Phe Leu Asp Gly Glu Asp
225 230 235 240
Pro Ser Glu Thr Ser Tyr Gly Gly Asp Leu Phe Glu Lys Ser Glu Glu
245 250 255
Asn Asn Cys Val Glu Trp Leu Asn Ser Lys Pro Lys Ser Ser Val Val
260 265 270
Tyr Val Ser Phe Gly Ser Val Leu Arg Phe Pro Lys Ala Gln Met Glu
275 280 285
Glu Ile Gly Lys Gly Leu Leu Ala Cys Gly Arg Pro Phe Leu Trp Met
290 295 300
Ile Arg Glu Gln Lys Asn Asp Asp Gly Glu Glu Glu Glu Glu Glu Glu
305 310 315 320
Glu Leu Ser Cys Ile Gly Glu Leu Lys Lys Met Gly Lys Ile Val Ser
325 330 335
Trp Cys Ser Gln Leu Glu Val Leu Ala His Pro Ala Leu Gly Cys Phe
340 345 350
Val Thr His Cys Gly Trp Asn Ser Ala Val Glu Ser Leu Ser Cys Gly
355 360 365
Ile Pro Val Val Ala Val Pro Gln Trp Phe Asp Gln Thr Thr Asn Ala
370 375 380
Lys Leu Ile Glu Asp Ala Trp Gly Thr Gly Val Arg Val Arg Met Asn
385 390 395 400
Glu Gly Gly Gly Val Asp Gly Cys Glu Ile Glu Arg Cys Val Glu Met
405 410 415
Val Met Asp Gly Gly Asp Lys Thr Lys Leu Val Arg Glu Asn Ala Ile
420 425 430
Lys Trp Lys Thr Leu Ala Arg Gln Ala Met Gly
435 440 443

<210> 9
<211> 461
<212> PRT
<213> Verbena hybrida
<400> 9

Met Ser Arg Ala His Val Leu Leu Ala Thr Phe Pro Ala Gln Gly His
1 5 10 15
Ile Asn Pro Ala Leu Gln Phe Ala Lys Arg Leu Ala Asn Ala Asp Ile
20 25 30
Gln Val Thr Phe Phe Thr Ser Val Tyr Ala Trp Arg Arg Met Ser Arg
35 40 45
Thr Ala Ala Gly Ser Asn Gly Leu Ile Asn Phe Val Ser Phe Ser Asp
50 55 60
Gly Tyr Asp Asp Gly Leu Gln Pro Gly Asp Asp Gly Lys Asn Tyr Met
65 70 75 80
Ser Glu Met Lys Ser Arg Gly Ile Lys Ala Leu Ser Asp Thr Leu Ala
85 90 95
Ala Asn Asn Val Asp Gln Lys Ser Ser Lys Ile Thr Phe Val Val Tyr
100 105 110
Ser His Leu Phe Ala Trp Ala Ala Lys Val Ala Arg Glu Phe His Leu
115 120 125
Arg Ser Ala Leu Leu Trp Ile Glu Pro Ala Thr Val Leu Asp Ile Phe
130 135 140
Tyr Phe Tyr Phe Asn Gly Tyr Ser Asp Glu Ile Asp Ala Gly Ser Asp
145 150 155 160
Ala Ile His Leu Pro Gly Gly Leu Pro Val Leu Ala Gln Arg Asp Leu
165 170 175
Pro Ser Phe Leu Leu Pro Ser Thr His Glu Arg Phe Arg Ser Leu Met
180 185 190
Lys Glu Lys Leu Glu Thr Leu Glu Gly Glu Glu Lys Pro Lys Val Leu
195 200 205
Val Asn Ser Phe Asp Ala Leu Glu Pro Asp Ala Leu Lys Ala Ile Asp
210 215 220
Lys Tyr Glu Met Ile Ala Ile Gly Pro Leu Ile Pro Ser Ala Phe Leu
225 230 235 240
Asp Gly Lys Asp Pro Ser Asp Arg Ser Phe Gly Gly Asp Leu Phe Glu
245 250 255
Lys Gly Ser Asn Asp Asp Asp Cys Leu Glu Trp Leu Ser Thr Asn Pro
260 265 270

Arg Ser Ser Val Val Tyr Val Ser Phe Gly Ser Phe Val Asn Thr Thr
275 280 285
Lys Ser Gln Met Glu Glu Ile Ala Arg Gly Leu Leu Asp Cys Gly Arg
290 295 300
Pro Phe Leu Trp Val Val Arg Val Asn Glu Gly Glu Glu Val Leu Ile
305 310 315 320
Ser Cys Met Glu Glu Leu Lys Arg Val Gly Lys Ile Val Ser Trp Cys
325 330 335
Ser Gln Leu Glu Val Leu Thr His Pro Ser Leu Gly Cys Phe Val Thr
340 345 350
His Cys Gly Trp Asn Ser Thr Leu Glu Ser Ile Ser Phe Gly Val Pro
355 360 365
Met Val Ala Phe Pro Gln Trp Phe Asp Gln Gly Thr Asn Ala Lys Leu
370 375 380
Met Glu Asp Val Trp Arg Thr Gly Val Arg Val Arg Ala Asn Glu Glu
385 390 395 400
Gly Ser Val Val Asp Gly Asp Glu Ile Arg Arg Cys Ile Glu Glu Val
405 410 415
Met Asp Gly Gly Glu Lys Ser Arg Lys Leu Arg Glu Ser Ala Gly Lys
420 425 430
Trp Lys Asp Leu Ala Arg Lys Ala Met Glu Glu Asp Gly Ser Ser Val
435 440 445
Asn Asn Leu Lys Val Phe Leu Asp Glu Val Val Gly Ile
450 455 460 461

<210> 10
<211> 478
<212> PRT
<213> Torenia hybrida
<220>
<221>
<222>
<223> Xaa (64) is Cys or Phe, Xaa (65) is Ser or Pro.
<400> 10
Met Val Asn Lys Arg His Ile Leu Leu Ala Thr Phe Pro Ala Gln Gly
1 5 10 15

His Ile Asn Pro Ser Leu Glu Phe Ala Lys Arg Leu Leu Asn Thr Gly
20 25 30
Tyr Val Asp Gln Val Thr Phe Phe Thr Ser Val Tyr Ala Leu Arg Arg
35 40 45
Met Arg Phe Glu Thr Asp Pro Ser Ser Arg Ile Asp Phe Val Ala Xaa
50 55 60
Xaa Asp Ser Tyr Asp Asp Gly Leu Lys Lys Gly Asp Asp Gly Lys Asn
65 70 75 80
Tyr Met Ser Glu Met Arg Lys Arg Gly Thr Lys Ala Leu Lys Asp Thr
85 90 95
Leu Ile Lys Leu Asn Asp Ala Ala Met Gly Ser Glu Cys Tyr Asn Arg
100 105 110
Val Ser Phe Val Val Tyr Ser His Leu Phe Ser Trp Ala Ala Glu Val
115 120 125
Ala Arg Glu Val Asp Val Pro Ser Ala Leu Leu Trp Ile Glu Pro Ala
130 135 140
Thr Val Phe Asp Val Tyr Tyr Phe Tyr Phe Asn Gly Tyr Ala Asp Asp
145 150 155 160
Ile Asp Ala Gly Ser Asp Gln Ile Gln Leu Pro Asn Leu Pro Gln Leu
165 170 175
Ser Lys Gln Asp Leu Pro Ser Phe Leu Leu Pro Ser Ser Pro Ala Arg
180 185 190
Phe Arg Thr Leu Met Lys Glu Lys Phe Asp Thr Leu Asp Lys Glu Pro
195 200 205
Lys Ala Lys Val Leu Ile Asn Thr Phe Asp Ala Leu Glu Thr Glu Gln
210 215 220
Leu Lys Ala Ile Asp Arg Tyr Glu Leu Ile Ser Ile Gly Pro Leu Ile
225 230 235 240

Pro Ser Ser Ile Phe Ser Asp Gly Asn Asp Pro Ser Ser Ser Asn Lys
245 250 255
Ser Tyr Gly Gly Asp Leu Phe Arg Lys Ala Asp Glu Thr Tyr Met Asp
260 265 270
Trp Leu Asn Ser Lys Pro Glu Ser Ser Val Val Tyr Val Ser Phe Gly
275 280 285

Ser Leu Leu Arg Leu Pro Lys Pro Gln Met Glu Glu Ile Ala Ile Gly
290 295 300
Leu Ser Asp Thr Lys Ser Pro Val Leu Trp Val Ile Arg Arg Asn Glu
305 310 315 320
Glu Gly Asp Glu Gln Glu Gln Ala Glu Glu Glu Glu Lys Leu Leu Ser
325 330 335
Phe Phe Asp Arg His Gly Thr Glu Arg Leu Gly Lys Ile Val Thr Trp
340 345 350
Cys Ser Gln Leu Asp Val Leu Thr His Lys Ser Val Gly Cys Phe Val
355 360 365
Thr His Cys Gly Trp Asn Ser Ala Ile Glu Ser Leu Ala Cys Gly Val
370 375 380
Pro Val Val Cys Phe Pro Gln Trp Phe Asp Gln Gly Thr Asn Ala Lys
385 390 395 400
Met Ile Glu Asp Val Trp Arg Ser Gly Val Arg Val Arg Val Asn Glu
405 410 415
Glu Gly Gly Val Val Asp Arg Arg Glu Ile Lys Arg Cys Val Ser Glu
420 425 430
Val Ile Lys Ser Arg Glu Leu Arg Glu Ser Ala Met Met Trp Lys Gly
435 440 445
Leu Ala Lys Glu Ala Met Asp Glu Glu Arg Gly Ser Ser Met Asn Asn
450 455 460
Leu Lys Asn Phe Ile Thr Arg Ile Ile Asn Glu Asn Ala Ser
465 470 475 478

<210> 11
<211> 335
<212> PRT
<213> Perilla frutescens
<400> 11

Met Ser Ser Ser Ser Ser Arg Arg Trp Arg Glu Asn Glu Gly Met Arg
1 5 10 15
Arg Thr Leu Leu Gly Leu Gly Leu Gly Gln Leu Val Ser Phe Asp Leu
20 25 30
Ala Ile Met Thr Phe Ser Ala Ser Leu Val Ser Thr Thr Val Asp Ala
35 40 45

Pro Leu Thr Met Ser Phe Thr Thr Tyr Thr Val Val Ala Leu Leu Tyr
50 55 60
Gly Thr Ile Leu Leu Tyr Arg Arg His Lys Phe Leu Val Pro Trp Tyr
65 70 75 80
Trp Tyr Ala Leu Leu Gly Phe Val Asp Val His Gly Asn Tyr Leu Val
85 90 95
Asn Lys Ala Phe Glu Leu Thr Ser Ile Thr Ser Val Ser Ile Leu Asp
100 105 110
Cys Trp Thr Ile Val Trp Ser Ile Ile Phe Thr Trp Met Phe Leu Gly
115 120 125
Thr Lys Tyr Ser Val Tyr Gln Phe Val Gly Ala Ala Ile Cys Val Gly
130 135 140
Gly Leu Leu Leu Val Leu Leu Ser Asp Ser Gly Val Thr Ala Ala Gly
145 150 155 160
Ser Asn Pro Leu Leu Gly Asp Phe Leu Val Ile Thr Gly Ser Ile Leu
165 170 175
Phe Thr Leu Ser Thr Val Gly Gln Glu Tyr Cys Val Lys Arg Lys Asp
180 185 190
Arg Ile Glu Val Val Ala Met Ile Gly Val Phe Gly Met Leu Ile Ser
195 200 205
Ala Thr Glu Ile Thr Val Leu Glu Arg Asn Ala Leu Ser Ser Met Gln
210 215 220
Trp Ser Thr Gly Leu Leu Ala Ala Tyr Val Val Tyr Ala Leu Ser Ser
225 230 235 240
Phe Leu Phe Cys Thr Leu Thr Pro Phe Leu Leu Lys Met Ser Gly Ala
245 250 255
Ala Phe Phe Asn Leu Ser Met Leu Thr Ser Asp Met Trp Ala Val Ala
260 265 270
Ile Arg Thr Phe Ile Tyr Asn Gln Glu Val Asp Trp Leu Tyr Tyr Leu
275 280 285
Ala Phe Cys Leu Val Val Val Gly Ile Phe Ile Tyr Thr Lys Thr Glu
290 295 300
Lys Asp Pro Asn Asn Thr Arg Ala Leu Glu Asn Gly Asn Leu Asp His
305 310 315 320
Glu Tyr Ser Leu Leu Glu Asp Gln Asp Asp Thr Pro Arg Lys Pro
325 330 335

<210> 12

<211> 468

<212> PRT

<213> Petunia hybrida

<400> 12

Met Val Gln Pro His Val Ile Leu Thr Thr Phe Pro Ala Gln Gly His
1 5 10 15

Ile Asn Pro Ala Leu Gln Phe Ala Lys Asn Leu Val Lys Met Gly Ile
20 25 30

Glu Val Thr Phe Ser Thr Ser Ile Tyr Ala Gln Ser Arg Met Asp Glu
35 40 45

Lys Ser Ile Leu Asn Ala Pro Lys Gly Leu Asn Phe Ile Pro Phe Ser
50 55 60

Asp Gly Phe Asp Glu Gly Phe Asp His Ser Lys Asp Pro Val Phe Tyr
65 70 75 80

Met Ser Gln Leu Arg Lys Cys Gly Ser Glu Thr Val Lys Lys Ile Ile
85 90 95

Leu Thr Cys Ser Glu Asn Gly Gln Pro Ile Thr Cys Leu Leu Tyr Ser
100 105 110

Ile Phe Leu Pro Trp Ala Ala Glu Val Ala Arg Glu Val His Ile Pro
115 120 125

Ser Ala Leu Leu Trp Ser Gln Pro Ala Thr Ile Leu Asp Ile Tyr Tyr
130 135 140

Phe Asn Phe His Gly Tyr Glu Lys Ala Met Ala Asn Glu Ser Asn Asp
145 150 155 160

Pro Asn Trp Ser Ile Gln Leu Pro Gly Leu Pro Leu Leu Glu Thr Arg
165 170 175

Asp Leu Pro Ser Phe Leu Leu Pro Tyr Gly Ala Lys Gly Ser Leu Arg
180 185 190

Val Ala Leu Pro Pro Phe Lys Glu Leu Ile Asp Thr Leu Asp Ala Glu
195 200 205

Thr Thr Pro Lys Ile Leu Val Asn Thr Phe Asp Glu Leu Glu Pro Glu
210 215 220

Ala Leu Asn Ala Ile Glu Gly Tyr Lys Phe Tyr Gly Ile Gly Pro Leu
225 230 235 240

Ile Pro Ser Ala Phe Leu Gly Gly Asn Asp Pro Leu Asp Ala Ser Phe
245 250 255

Gly Gly Asp Leu Phe Gln Asn Ser Asn Asp Tyr Met Glu Trp Leu Asn
260 265 270

Ser Lys Pro Asn Ser Ser Val Val Tyr Ile Ser Phe Gly Ser Leu Met
275 280 285
Asn Pro Ser Ile Ser Gln Met Glu Glu Ile Ser Lys Gly Leu Ile Asp
290 295 300
Ile Gly Arg Pro Phe Leu Trp Val Ile Lys Glu Asn Glu Lys Gly Lys
305 310 315 320
Glu Glu Glu Asn Lys Lys Leu Gly Cys Ile Glu Glu Leu Glu Lys Ile
325 330 335
Gly Lys Ile Val Pro Trp Cys Ser Gln Leu Glu Val Leu Lys His Pro
340 345 350
Ser Leu Gly Cys Phe Val Ser His Cys Gly Trp Asn Ser Ala Leu Glu
355 360 365
Ser Leu Ala Cys Gly Val Pro Val Val Ala Phe Pro Gln Trp Thr Asp
370 375 380
Gln Met Thr Asn Ala Lys Gln Val Glu Asp Val Trp Lys Ser Gly Val
385 390 395 400
Arg Val Arg Ile Asn Glu Asp Gly Val Val Glu Ser Glu Glu Ile Lys
405 410 415
Arg Cys Ile Glu Leu Val Met Asp Gly Gly Glu Lys Gly Glu Glu Leu
420 425 430
Arg Lys Asn Ala Lys Lys Trp Lys Glu Leu Ala Arg Glu Ala Val Lys
435 440 445
Glu Gly Gly Ser Ser His Lys Asn Leu Lys Ala Phe Ile Asp Asp Val
450 455 460
Ala Lys Gly Phe
465 468

Sequence

Sequence ID No.: 1

Sequence length: 1507

Sequence type: Nucleic acid

Number of strands: Double-strand

Topology: Straight chain

Source:

Biological name: Perilla (Perilla frutescens)

Tissue type: Leaf

Direct source:

Library name: cDNA library

Clone name: p3R4

Sequence:

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GAAAATTTCC ACAAAA ATG GTC CGC CGC CGC GTG CTG CTA GCA ACG TTT      49
                   Met Val Arg Arg Arg Val Leu Leu Ala Thr Phe
                     1               5                  10
CCT GCG CAA GGC CAC ATA AAT CCC GCC CTC CAA TTC GCC AAG AGA CTC    97
Pro Ala Gln Gly His Ile Asn Pro Ala Leu Gln Phe Ala Lys Arg Leu
               15                  20                  25
CTA AAA GCC GGC ACT GAC GTC ACA TTT TTC ACG AGC GTT TAT GCA TGG   145
Leu Lys Ala Gly Thr Asp Val Thr Phe Phe Thr Ser Val Tyr Ala Trp
          30                  35                  40
CGC CGC ATG GCC AAC ACA GCC TCC GCC GCT GCC GGA AAC CCA CCG GGC   193
Arg Arg Met Ala Asn Thr Ala Ser Ala Ala Ala Gly Asn Pro Pro Gly
     45                  50                  55
CTC GAC TTC GTG GCG TTC TCC GAC GGC TAC GAC GAC GGG CTG AAG CCC   241
Leu Asp Phe Val Ala Phe Ser Asp Gly Tyr Asp Asp Gly Leu Lys Pro
 60                  65                  70                  75
TGC GGC GAC GGG AAG CGC TAC ATG TCC GAG ATG AAA GCC CGC GGC TCC   289
Cys Gly Asp Gly Lys Arg Tyr Met Ser Glu Met Lys Ala Arg Gly Ser
                 80                  85                  90
GAG GCC TTA AGA AAC CTC CTT CTC AAC AAC CAC GAC GTC ACG TTC GTC   337
Glu Ala Leu Arg Asn Leu Leu Leu Asn Asn His Asp Val Thr Phe Val
             95                  100                 105
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GTC TAC TCC CAC CTC TTT GCA TGG GCG GCG GAG GTG GCG CGT GAG TCC     385
Val Tyr Ser His Leu Phe Ala Trp Ala Ala Glu Val Ala Arg Glu Ser
        110                 115                 120
CAG GTC CCG AGC GCC CTT CTC TGG GTC GAG CCC GCC ACC GTG CTG TGC     433
Gln Val Pro Ser Ala Leu Leu Trp Val Glu Pro Ala Thr Val Leu Cys
    125                 130                 135
ATA TAT TAC TTC TAC TTC AAC GGC TAC GCA GAC GAG ATC GAC GCC GGT     481
Ile Tyr Tyr Phe Tyr Phe Asn Gly Tyr Ala Asp Glu Ile Asp Ala Gly
140                 145                 150                 155
TCC GAC GAA ATT CAG CTC CCT CGG CTT CCA CCC CTG GAG CAG CGC AGT     529
Ser Asp Glu Ile Gln Leu Pro Arg Leu Pro Pro Leu Glu Gln Arg Ser
                160                 165                 170
CTT CCG ACC TTT CTG CTG CCG GAG ACA CCG GAG AGA TTC CGG TTG ATG     577
Leu Pro Thr Phe Leu Leu Pro Glu Thr Pro Glu Arg Phe Arg Leu Met
            175                 180                 185
ATG AAG GAG AAG CTG GAA ACT TTA GAC GGT GAA GAG AAG GCG AAA GTG     625
Met Lys Glu Lys Leu Glu Thr Leu Asp Gly Glu Glu Lys Ala Lys Val
        190                 195                 200
TTG GTG AAC ACG TTT GAT GCG TTG GAG CCC GAT GCA CTC ACG GCT ATT     673
Leu Val Asn Thr Phe Asp Ala Leu Glu Pro Asp Ala Leu Thr Ala Ile
    205                 210                 215
GAT AGG TAT GAG TTG ATC GGG ATC GGG CCG TTG ATT CCC TCC GCC TTC     721
Asp Arg Tyr Glu Leu Ile Gly Ile Gly Pro Leu Ile Pro Ser Ala Phe
220                 225                 230                 235
TTG GAC GGC GGA GAT CCC TCC GAA ACG TCT TAC GGC GGC GAT CTT TTC     769
Leu Asp Gly Gly Asp Pro Ser Glu Thr Ser Tyr Gly Gly Asp Leu Phe
                240                 245                 250
GAA AAA TCG GAG GAG AAT AAC TGC GTG GAG TGG TTG GAC ACG AAG CCG     817
Glu Lys Ser Glu Glu Asn Asn Cys Val Glu Trp Leu Asp Thr Lys Pro
            255                 260                 265
AAA TCT TCG GTG GTG TAT GTG TCG TTT GGG AGC GTT TTG AGG TTT CCA     865
Lys Ser Ser Val Val Tyr Val Ser Phe Gly Ser Val Leu Arg Phe Pro
        270                 275                 280
AAG GCA CAA ATG GAA GAG ATT GGG AAA GGG CTA TTA GCC TGC GGA AGG     913
Lys Ala Gln Met Glu Glu Ile Gly Lys Gly Leu Leu Ala Cys Gly Arg
    285                 290                 295
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CCG TTT TTA TGG ATG ATA CGA GAA CAG AAG AAT GAC GAC GGC GAA GAA     961
Pro Phe Leu Trp Met Ile Arg Glu Gln Lys Asn Asp Asp Gly Glu Glu
300                 305                 310                 315
GAA GAA GAA GAG TTG AGT TGC ATT GGG GAA TTG AAA AAA ATG GGG AAA    1009
Glu Glu Glu Glu Leu Ser Cys Ile Gly Glu Leu Lys Lys Met Gly Lys
                320                 325                 330
ATA GTT TCG TGG TGC TCG CAG TTG GAG GTT CTG GCG CAC CCT GCG TTG    1057
Ile Val Ser Trp Cys Ser Gln Leu Glu Val Leu Ala His Pro Ala Leu
            335                 340                 345
GGA TGT TTC GTG ACG CAT TGT GGG TGG AAC TCG GCT GTG GAG AGC TTG    1105
Gly Cys Phe Val Thr His Cys Gly Trp Asn Ser Ala Val Glu Ser Leu
        350                 355                 360
AGT TGC GGG GTT CCG GTG GTG GCG GTG CCG CAG TGG TTT GAT CAG ACG    1153
Ser Cys Gly Val Pro Val Val Ala Val Pro Gln Trp Phe Asp Gln Thr
    365                 370                 375
ACG AAT GCG AAG CTG ATT GAG GAT GCG TGG GGG ACA GGG GTG AGA GTG    1201
Thr Asn Ala Lys Leu Ile Glu Asp Ala Trp Gly Thr Gly Val Arg Val
380                 385                 390                 395
AGA ATG AAT GAA GGG GGT GGG GTT GAT GGA TCT GAG ATA GAG AGG TGT    1249
Arg Met Asn Glu Gly Gly Gly Val Asp Gly Ser Glu Ile Glu Arg Cys
                400                 405                 410
GTG GAG ATG GTG ATG GAT GGG GGT GAG AAG AGC AAA CTA GTG AGA GAA    1297
Val Glu Met Val Met Asp Gly Gly Glu Lys Ser Lys Leu Val Arg Glu
            415                 420                 425
AAT GCC ATA AAA TGG AAG ACT TTG GCC AGA GAA GCC ATG GGA GAG GAT    1345
Asn Ala Ile Lys Trp Lys Thr Leu Ala Arg Glu Ala Met Gly Glu Asp
        430                 435                 440
GGA TCT TCA CTC AAG AAT CTC AAC GCC TTT CTT CAT CAA GTT GCA CGT    1393
Gly Ser Ser Leu Lys Asn Leu Asn Ala Phe Leu His Gln Val Ala Arg
    445                 450                 455
GCT TAATACACAA AATGGCTTTC CACTTTTAAT CTACTCAAAC ACCGGTTCAA         1446
Ala
460                                                               1507
ATAAATATCC CCTTCCACTT CTTTCTATTT CACTATCACA TTTATAATTT TAGTAACAAA 1506
A
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Sequence ID No.: 2

Sequence length: 1470

Sequence type: Nucleic acid
Number of strands: Double-strand
Topology: Straight chain
Source:
Biological name: Perilla (Perilla frutescens)
Tissue type: Leaf
Direct source:
Library name: cDNA library
Clone name: p3R6
Sequence:

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ACCAAACCAA AACAAAATTT CCACAAAA ATG GTC CGC CGC CGC GTG CTG CTA      48
                               Met Val Arg Arg Arg Val Leu Leu
                                 1               5

GCA ACG TTT CCG GCG CAA GGC CAC ATA AAT CCC GCC CTC CAA TTC GCC     96
Ala Thr Phe Pro Ala Gln Gly His Ile Asn Pro Ala Leu Gln Phe Ala
     10                  15                  20

AAG AGA CTC CTA AAA GCC GGC ACT GAC GTC ACG TTT TTC ACG AGC GTT    144
Lys Arg Leu Leu Lys Ala Gly Thr Asp Val Thr Phe Phe Thr Ser Val
 25                  30                  35                  40

TAT GCA TGG CGC CGC ATG GCC AAC ACA GCC TCC GCC GCT GCC GGA AAC    192
Tyr Ala Trp Arg Arg Met Ala Asn Thr Ala Ser Ala Ala Ala Gly Asn
                    45                  50                  55

CCA CCG GGC CTC GAC TTC GTG GCG TTC TCC GAC GGC TAC GAC GAC GGG    240
Pro Pro Gly Leu Asp Phe Val Ala Phe Ser Asp Gly Tyr Asp Asp Gly
                60                  65                  70

CTG AAG CCC GGC GGC GAC GGG AAG CGC TAC ATG TCC GAG ATG AAA GCC    288
Leu Lys Pro Gly Gly Asp Gly Lys Arg Tyr Met Ser Glu Met Lys Ala
          75                  80                  85

CGC GGC TCC GAG GCC TTA AGA AAC CTC CTT CTC AAC AAC GAC GAC GTC    336
Arg Gly Ser Glu Ala Leu Arg Asn Leu Leu Leu Asn Asn Asp Asp Val
     90                  95                  100

ACT TTC GTC GTC TAC TCC CAC CTC TTT GCA TGG GCG GCG GAG GTG GCG    384
Thr Phe Val Val Tyr Ser His Leu Phe Ala Trp Ala Ala Glu Val Ala
105                 110                 115                 120
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```
CGT TTG TCC CAC GTC CCG ACC GCC CTT CTC TGG GTC GAG CCC GCC ACC     432
Arg Leu Ser His Val Pro Thr Ala Leu Leu Trp Val Glu Pro Ala Thr
                125                 130                 135
GTG CTG TGC ATA TAC CAC TTC TAC TTC AAC GGC TAC GCA GAC GAG ATC     480
Val Leu Cys Ile Tyr His Phe Tyr Phe Asn Gly Tyr Ala Asp Glu Ile
            140                 145                 150
GAC GCC GGT TCC AAT GAA ATT CAG CTC CCT CGG CTT CCA TCC CTG GAG     528
Asp Ala Gly Ser Asn Glu Ile Gln Leu Pro Arg Leu Pro Ser Leu Glu
        155                 160                 165
CAG CGC AGT CTT CCG ACG TTT CTG CTG CCT GCG ACG CCG GAG AGA TTC     576
Gln Arg Ser Leu Pro Thr Phe Leu Leu Pro Ala Thr Pro Glu Arg Phe
    170                 175                 180
CGG TTG ATG ATG AAG GAG AAG CTG GAA ACT TTA GAC GGT GAA GAG AAG     624
Arg Leu Met Met Lys Glu Lys Leu Glu Thr Leu Asp Gly Glu Glu Lys
185                 190                 195                 200
GCG AAA GTA TTG GTG AAC ACG TTT GAT GCG TTG GAG CCC GAT GCA CTC     672
Ala Lys Val Leu Val Asn Thr Phe Asp Ala Leu Glu Pro Asp Ala Leu
                205                 210                 215
ACG GCT ATT GAT AGG TAT GAG TTG ATC GGG ATC GGG CCG TTG ATT CCC     720
Thr Ala Ile Asp Arg Tyr Glu Leu Ile Gly Ile Gly Pro Leu Ile Pro
            220                 225                 230
TCC GCC TTC TTG GAC GGC GAA GAT CCC TCC GAA ACG TCT TAC GGC GGC     768
Ser Ala Phe Leu Asp Gly Glu Asp Pro Ser Glu Thr Ser Tyr Gly Gly
        235                 240                 245
GAT CTT TTC GAA AAA TCG GAG GAG AAT AAC TGC GTG GAG TGG TTG AAC     816
Asp Leu Phe Glu Lys Ser Glu Glu Asn Asn Cys Val Glu Trp Leu Asn
    250                 255                 260
TCG AAG CCG AAA TCT TCG GTG GTG TAT GTG TCG TTT GGG AGC GTT TTG     864
Ser Lys Pro Lys Ser Ser Val Val Tyr Val Ser Phe Gly Ser Val Leu
265                 270                 275                 280
AGG TTT CCA AAG GCA CAA ATG GAA GAG ATT GGG AAA GGG CTA TTA GCC     912
Arg Phe Pro Lys Ala Gln Met Glu Glu Ile Gly Lys Gly Leu Leu Ala
                285                 290                 295
TGC GGA AGG CCC TTT TTA TGG ATG ATA CGA GAA CAG AAG AAT GAC GAC     960
Cys Gly Arg Pro Phe Leu Trp Met Ile Arg Glu Gln Lys Asn Asp Asp
            300                 305                 310
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GGC GAA GAA GAA GAA GAA GAA GAA GAG TTG AGT TGC ATT GGG GAA TTG   1008
Gly Glu Glu Glu Glu Glu Glu Glu Glu Leu Ser Cys Ile Gly Glu Leu
        315                 320                 325
AAA AAA ATG GGG AAA ATA GTG TCG TGG TGC TCG CAG TTG GAG GTT CTG   1056
Lys Lys Met Gly Lys Ile Val Ser Trp Cys Ser Gln Leu Glu Val Leu
    330                 335                 340
GCG CAC CCT GCG TTG GGA TGT TTC GTG ACG CAT TGT GGG TGG AAC TCG   1104
Ala His Pro Ala Leu Gly Cys Phe Val Thr His Cys Gly Trp Asn Ser
345                 350                 355                 360
GCT GTG GAG AGC TTG AGT TGC GGG ATT CCG GTG GTG GCG GTG CCG CAG   1152
Ala Val Glu Ser Leu Ser Cys Gly Ile Pro Val Val Ala Val Pro Gln
                365                 370                 375
TGG TTT GAT CAG ACG ACG AAT GCG AAG CTG ATT GAG GAT GCG TGG GGG   1200
Trp Phe Asp Gln Thr Thr Asn Ala Lys Leu Ile Glu Asp Ala Trp Gly
            380                 385                 390
ACA GGG GTG AGA GTG AGA ATG AAT GAA GGG GGT GGG GTT GAT GGA TGT   1248
Thr Gly Val Arg Val Arg Met Asn Glu Gly Gly Gly Val Asp Gly Cys
        395                 400                 405
GAG ATA GAA AGG TGT GTG GAG ATG GTG ATG GAT GGG GGT GAC AAG ACC   1296
Glu Ile Glu Arg Cys Val Glu Met Val Met Asp Gly Gly Asp Lys Thr
    410                 415                 420
AAA CTA GTG AGA GAA AAT GCC ATC AAA TGG AAG ACT TTG GCC AGA CAA   1344
Lys Leu Val Arg Glu Asn Ala Ile Lys Trp Lys Thr Leu Ala Arg Gln
425                 430                 435                 440
GCC ATG GGA TAGGATGGAT CTTCACTCAA CAATCTCAAC GCCTTTCTTC           1393
Ala Met Gly
        443
GTCAAGTTGC ACACTTTTAA TCTGCTCAAA CAGCGGTTCA AATAAATATC CCCTTCCACT 1453
TAAAAAAAAA AAAAAAA                                               1470
```

Sequence ID No.: 3

Sequence length: 2062

Sequence type: Nucleic acid

Number of strands: Double-strand

Topology: Straight chain

Source:

Biological name: Verbena (Verbena hybrida)

Tissue type: Petal

Direct source:

Library name: cDNA library

Clone name: pSHGT8

Sequence:

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ATTTTACCAA AAAAATAAAA AAAAA ATG AGC AGA GCT CAC GTC CTC TTG GCC      52
                            Met Ser Arg Ala His Val Leu Leu Ala
                              1               5

ACA TTC CCA GCA CAG GGA CAC ATA AAT CCC GCC CTT CAA TTC GCC AAG     100
Thr Phe Pro Ala Gln Gly His Ile Asn Pro Ala Leu Gln Phe Ala Lys
 10                  15                  20                  25

CGT CTC GCA AAT GCC GAC ATT CAA GTC ACA TTC TTC ACC AGC GTC TAC     148
Arg Leu Ala Asn Ala Asp Ile Gln Val Thr Phe Phe Thr Ser Val Tyr
                 30                  35                  40

GCA TGG CGC CGC ATG TCC AGA ACC GCC GCT GGC TCA AAC GGG CTC ATC     196
Ala Trp Arg Arg Met Ser Arg Thr Ala Ala Gly Ser Asn Gly Leu Ile
             45                  50                  55

AAT TTT GTG TCG TTT TCC GAC GGG TAT GAC GAC GGG TTA CAG CCC GGA     244
Asn Phe Val Ser Phe Ser Asp Gly Tyr Asp Asp Gly Leu Gln Pro Gly
         60                  65                  70

GAC GAT GGG AAG AAC TAC ATG TCG GAG ATG AAA AGC AGA GGT ATA AAA     292
Asp Asp Gly Lys Asn Tyr Met Ser Glu Met Lys Ser Arg Gly Ile Lys
     75                  80                  85

GCC TTG AGC GAT ACT CTT GCA GCC AAT AAT GTC GAT CAA AAA AGC AGC     340
Ala Leu Ser Asp Thr Leu Ala Ala Asn Asn Val Asp Gln Lys Ser Ser
90                  95                 100                 105

AAA ATC ACG TTC GTG GTG TAC TCC CAC CTC TTT GCA TGG GCG GCC AAG     388
Lys Ile Thr Phe Val Val Tyr Ser His Leu Phe Ala Trp Ala Ala Lys
                110                 115                 120

GTG GCG CGT GAG TTC CAT CTC CGG AGC GCG CTA CTC TGG ATT GAG CCA     436
Val Ala Arg Glu Phe His Leu Arg Ser Ala Leu Leu Trp Ile Glu Pro
            125                 130                 135

GCT ACG GTG TTG GAT ATA TTT TAC TTT TAT TTC AAC GGC TAT AGC GAC     484
Ala Thr Val Leu Asp Ile Phe Tyr Phe Tyr Phe Asn Gly Tyr Ser Asp
        140                 145                 150
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GAA ATC GAT GCG GGT TCG GAT GCT ATT CAC TTG CCC GGA GGA CTC CCA     532
Glu Ile Asp Ala Gly Ser Asp Ala Ile His Leu Pro Gly Gly Leu Pro
    155                 160                 165
GTG CTG GCC CAG CGT GAT TTA CCG TCT TTC CTT CTT CCT TCC ACG CAT     580
Val Leu Ala Gln Arg Asp Leu Pro Ser Phe Leu Leu Pro Ser Thr His
170                 175                 180                 185
GAG AGA TTC CGT TCA CTG ATG AAG GAG AAA TTG GAA ACT TTA GAA GGT     628
Glu Arg Phe Arg Ser Leu Met Lys Glu Lys Leu Glu Thr Leu Glu Gly
                190                 195                 200
GAA GAA AAA CCT AAG GTC TTG GTG AAC AGC TTT GAT GCG TTG GAG CCT     676
Glu Glu Lys Pro Lys Val Leu Val Asn Ser Phe Asp Ala Leu Glu Pro
            205                 210                 215
GAT GCG CTC AAG GCC ATT GAT AAG TAC GAG ATG ATT GCA ATC GGG CCG     724
Asp Ala Leu Lys Ala Ile Asp Lys Tyr Glu Met Ile Ala Ile Gly Pro
        220                 225                 230
TTG ATT CCT TCC GCA TTC TTG GAC GGT AAA GAT CCT TCG GAC AGG TCT     772
Leu Ile Pro Ser Ala Phe Leu Asp Gly Lys Asp Pro Ser Asp Arg Ser
    235                 240                 245
TTC GGC GGA GAT TTG TTC GAG AAA GGG TCG AAT GAC GAC GAT TGC CTC     820
Phe Gly Gly Asp Leu Phe Glu Lys Gly Ser Asn Asp Asp Asp Cys Leu
250                 255                 260                 265
GAA TGG TTG AGC ACG AAT CCT CGA TCT TCG GTG GTT TAC GTT TCG TTC     868
Glu Trp Leu Ser Thr Asn Pro Arg Ser Ser Val Val Tyr Val Ser Phe
                270                 275                 280
GGA AGC TTC GTT AAT ACG ACG AAG TCG CAA ATG GAA GAG ATA GCA AGA     916
Gly Ser Phe Val Asn Thr Thr Lys Ser Gln Met Glu Glu Ile Ala Arg
            285                 290                 295
GGG CTG TTA GAT TGT GGG AGG CCG TTT TTG TGG GTG GTA AGA GTA AAC     964
Gly Leu Leu Asp Cys Gly Arg Pro Phe Leu Trp Val Val Arg Val Asn
        300                 305                 310
GAA GGA GAA GAG GTA TTG ATA AGT TGC ATG GAG GAG TTG AAA CGA GTG    1012
Glu Gly Glu Glu Val Leu Ile Ser Cys Met Glu Glu Leu Lys Arg Val
    315                 320                 325
GGG AAA ATT GTA TCT TGG TGT TCT CAA TTG GAA GTC CTG ACG CAT CCC    1060
Gly Lys Ile Val Ser Trp Cys Ser Gln Leu Glu Val Leu Thr His Pro
330                 335                 340                 345
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TCG TTG GGA TGT TTC GTG ACA CAC TGC GGG TGG AAT TCG ACT CTA GAG   1108
Ser Leu Gly Cys Phe Val Thr His Cys Gly Trp Asn Ser Thr Leu Glu
                350                 355                 360
AGT ATA TCT TTC GGG GTT CCG ATG GTG GCT TTT CCG CAG TGG TTC GAT   1156
Ser Ile Ser Phe Gly Val Pro Met Val Ala Phe Pro Gln Trp Phe Asp
            365                 370                 375
CAA GGG ACG AAT GCG AAG CTG ATG GAG GAT GTG TGG AGG ACG GGT GTG   1204
Gln Gly Thr Asn Ala Lys Leu Met Glu Asp Val Trp Arg Thr Gly Val
        380                 385                 390
AGA GTG AGA GCT AAT GAG GAG GGT AGC GTC GTT GAT GGT GAT GAA ATT   1252
Arg Val Arg Ala Asn Glu Glu Gly Ser Val Val Asp Gly Asp Glu Ile
    395                 400                 405
AGG AGA TGT ATT GAG GAG GTT ATG GAT GGG GGA GAA AAG AGT AGG AAA   1300
Arg Arg Cys Ile Glu Glu Val Met Asp Gly Gly Glu Lys Ser Arg Lys
410                 415                 420                 425
CTT AGA GAG AGT GCT GGC AAG TGG AAG GAT TTG GCA AGA AAA GCT ATG   1348
Leu Arg Glu Ser Ala Gly Lys Trp Lys Asp Leu Ala Arg Lys Ala Met
                430                 435                 440
GAG GAA GAT GGA TCT TCA GTT AAC AAC CTC AAG GTC TTT CTT GAT GAG   1396
Glu Glu Asp Gly Ser Ser Val Asn Asn Leu Lys Val Phe Leu Asp Glu
            445                 450                 455
GTT GTA GGT ATC TAAAGACGTA AATGAGGTCC CCATAGGCAA AATTGCAAAT       1448
Val Val Gly Ile
        460 461
TTCATCTCGT AAGTTGAATA CTTTTTGGCT TTAATTTTGT TCGAGTTTGT TTTTCAAAAT  1508
TTATCTTGTA ATTTTACATT GAGTGTAAAT TTAGTCTGAT TTTAACTGGA AAAATATAAA  1568
ATTCATTGTT GAGACTCTTC ATCAAAATCA TCTGATTTCC TTTATTGTCT TGGTCAAAAT  1628
TCTCATATCA ATTGGAAAAA ATAAATTTCA AAATCGTCCA ATTTTGAACC AAGAAAGAAG  1688
TATAATTTGA CCAAAATAAT AAAAGGATTC AAGTGATCTT GATGAAGTGT CTGAGCGACG  1748
AGTTCTATAT TTTTCCACCG AATTTCTAAC GAGTTTTTGA ATTTTTTTTA GCCAAAATCG  1808
GACTAACTTT GTACAAAATG AAAAGTTATA TGATGAAATT TTAAAAAACA AACTCAGACA  1868
ATAATAAAGC CCGAAAGTAG TAAAATTACC TGACGAAATT TGCAATTTCG CCTCCTATTT  1928
TAATTTTTTT GGTGTGTTTA ATAAATCGGT TATTTTACTT TTAATTAAAA TAAAAGTGAG  1988
ATGCATGATA GCTTGGTGAG TATATATGAG TTGATGGTAA TGTACGATAT TTTCTAAAAA  2048
AAAAAAAAAA AAAA                                                    2062
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Sequence ID No.: 4

Sequence length: 1671

Sequence type: Nucleic acid
Number of strands: Double-strand
Topology: Straight chain
Source:
Biological name: Trenia
Tissue type: Petal
Direct source:
Library name: cDNA library
Clone name: pSTGT5
Sequence:

```
AACACATAAA AAAAAAATAA AAGAAGAAAT AATTAAAAAA AAAA ATG GTT AAC        53
                                                     Met Val Asn
                                                       1

AAA CGC CAT ATT CTA CTA GCA ACA TTC CCA GCA CAA GGC CAC ATA AAC     101
Lys Arg His Ile Leu Leu Ala Thr Phe Pro Ala Gln Gly His Ile Asn
     5                  10                  15

CCT TCT CTC GAG TTC GCC AAA AGG CTC CTC AAC ACC GGA TAC GTC GAC     149
Pro Ser Leu Glu Phe Ala Lys Arg Leu Leu Asn Thr Gly Tyr Val Asp
 20                  25                  30                  35

CAA GTC ACA TTC TTC ACG AGT GTA TAC GCA TTG AGA CGC ATG CGC TTC     197
Gln Val Thr Phe Phe Thr Ser Val Tyr Ala Leu Arg Arg Met Arg Phe
                 40                  45                  50

GAA ACC GAT CCG AGC AGC AGA ATC GAT TTC GTG GCA TKT YCA GAT TCT     245
Glu Thr Asp Pro Ser Ser Arg Ile Asp Phe Val Ala Xaa Xaa Asp Ser
             55                  60                  65

TAC GAT GAT GGC TTA AAG AAA GGC GAC GAT GGC AAA AAC TAC ATG TCG     293
Tyr Asp Asp Gly Leu Lys Lys Gly Asp Asp Gly Lys Asn Tyr Met Ser
         70                  75                  80

GAG ATG AGA AAG CGC GGA ACG AAG GCC TTA AAG GAC ACT CTT ATT AAG     341
Glu Met Arg Lys Arg Gly Thr Lys Ala Leu Lys Asp Thr Leu Ile Lys
     85                  90                  95

CTC AAC GAT GCT GCG ATG GGA AGT GAA TGT TAC AAT CGC GTG AGC TTT     389
Leu Asn Asp Ala Ala Met Gly Ser Glu Cys Tyr Asn Arg Val Ser Phe
100                 105                 110                 115
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GTG GTG TAC TCT CAT CTA TTT TCG TGG GCA GCT GAA GTG GCG CGT GAA     437
Val Val Tyr Ser His Leu Phe Ser Trp Ala Ala Glu Val Ala Arg Glu
                    120                 125                 130
GTC GAC GTG CCG AGT GCC CTT CTT TGG ATT GAA CCG GCT ACG GTT TTC     485
Val Asp Val Pro Ser Ala Leu Leu Trp Ile Glu Pro Ala Thr Val Phe
                135                 140                 145
GAT GTG TAC TAT TTT TAC TTC AAT GGG TAT GCC GAT GAT ATC GAT GCG     533
Asp Val Tyr Tyr Phe Tyr Phe Asn Gly Tyr Ala Asp Asp Ile Asp Ala
        150                 155                 160
GGC TCA GAT CAA ATC CAA CTG CCC AAT CTT CCG CAG CTC TCC AAG CAA     581
Gly Ser Asp Gln Ile Gln Leu Pro Asn Leu Pro Gln Leu Ser Lys Gln
    165                 170                 175
GAT CTC CCC TCT TTC CTA CTC CCT TCG AGC CCC GCG AGA TTC CGA ACC     629
Asp Leu Pro Ser Phe Leu Leu Pro Ser Ser Pro Ala Arg Phe Arg Thr
180                 185                 190                 195
CTA ATG AAA GAA AAG TTC GAC ACG CTC GAC AAA GAA CCG AAA GCG AAG     677
Leu Met Lys Glu Lys Phe Asp Thr Leu Asp Lys Glu Pro Lys Ala Lys
                200                 205                 210
GTC TTG ATA AAC ACG TTC GAC GCA TTA GAA ACC GAA CAA CTC AAA GCC     725
Val Leu Ile Asn Thr Phe Asp Ala Leu Glu Thr Glu Gln Leu Lys Ala
            215                 220                 225
ATC GAC AGG TAT GAA CTA ATA TCC ATC GGC CCA TTA ATC CCA TCA TCG     773
Ile Asp Arg Tyr Glu Leu Ile Ser Ile Gly Pro Leu Ile Pro Ser Ser
        230                 235                 240
ATA TTC TCA GAT GGC AAC GAC CCC TCA TCA AGC AAC AAA TCC TAC GGT     821
Ile Phe Ser Asp Gly Asn Asp Pro Ser Ser Ser Asn Lys Ser Tyr Gly
    245                 250                 255
GGA GAC CTC TTC AGA AAA GCC GAT GAA ACT TAC ATG GAC TGG CTA AAC     869
Gly Asp Leu Phe Arg Lys Ala Asp Glu Thr Tyr Met Asp Trp Leu Asn
260                 265                 270                 275
TCA AAA CCC GAA TCA TCG GTC GTT TAC GTT TCG TTC GGG AGC CTC CTG     917
Ser Lys Pro Glu Ser Ser Val Val Tyr Val Ser Phe Gly Ser Leu Leu
                280                 285                 290
AGG CTC CCG AAA CCC CAA ATG GAA GAA ATA GCA ATA GGG CTT TCA GAC     965
Arg Leu Pro Lys Pro Gln Met Glu Glu Ile Ala Ile Gly Leu Ser Asp
            295                 300                 305
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ACC AAA TCG CCA GTT CTC TGG GTG ATA AGA AGA AAC GAA GAG GGC GAC   1013
Thr Lys Ser Pro Val Leu Trp Val Ile Arg Arg Asn Glu Glu Gly Asp
        310                 315                 320
GAA CAA GAG CAA GCA GAA GAA GAA GAG AAG CTG CTG AGC TTC TTT GAT   1061
Glu Gln Glu Gln Ala Glu Glu Glu Glu Lys Leu Leu Ser Phe Phe Asp
    325                 330                 335
CGT CAC GGA ACT GAA CGA CTC GGG AAA ATC GTG ACA TGG TGC TCA CAA   1109
Arg His Gly Thr Glu Arg Leu Gly Lys Ile Val Thr Trp Cys Ser Gln
340                 345                 350                 355
TTG GAT GTT CTG ACG CAT AAG TCG GTG GGA TGC TTC GTG ACG CAT TGC   1157
Leu Asp Val Leu Thr His Lys Ser Val Gly Cys Phe Val Thr His Cys
                360                 365                 370
GGT TGG AAT TCT GCT ATC GAG AGC CTG GCT TGT GGT GTG CCC GTG GTG   1205
Gly Trp Asn Ser Ala Ile Glu Ser Leu Ala Cys Gly Val Pro Val Val
            375                 380                 385
TGC TTT CCT CAA TGG TTC GAT CAA GGG ACT AAT GCG AAG ATG ATC GAA   1253
Cys Phe Pro Gln Trp Phe Asp Gln Gly Thr Asn Ala Lys Met Ile Glu
        390                 395                 400
GAT GTG TGG AGG AGT GGT GTG AGA GTC AGA GTG AAT GAG GAA GGC GGC   1301
Asp Val Trp Arg Ser Gly Val Arg Val Arg Val Asn Glu Glu Gly Gly
    405                 410                 415
GTT GTT GAT AGG CGT GAG ATT AAG AGG TGC GTC TCG GAG GTT ATA AAG   1349
Val Val Asp Arg Arg Glu Ile Lys Arg Cys Val Ser Glu Val Ile Lys
420                 425                 430                 435
AGT CGA GAG TTG AGA GAA AGC GCA ATG ATG TGG AAG GGT TTG GCT AAA   1397
Ser Arg Glu Leu Arg Glu Ser Ala Met Met Trp Lys Gly Leu Ala Lys
                440                 445                 450
GAA GCT ATG GAT GAA GAA CGT GGA TCA TCA ATG AAC AAT CTG AAG AAT   1445
Glu Ala Met Asp Glu Glu Arg Gly Ser Ser Met Asn Asn Leu Lys Asn
            455                 460                 465
TTT ATT ACT AGG ATT ATT AAT GAA AAT GCC TCA TAAGTTGTAC           1488
Phe Ile Thr Arg Ile Ile Asn Glu Asn Ala Ser
        470                 475         478
TATATATGTT ATTATTGTTG TTATGGACGT CGAATTAAGT ATTAGTTAAA TGATATGTAT  1548
TTAGAGGAAG GCCAAAACGG GCTACACCCG GCAGGCCACG GGTTGGAAAA GCCCGCCATG  1608
ATTTAAAATA TATATTTTAA AATAAATATT TTCTACTATT AAACTAAAAA AAAAAAAAAA  1668
AAA                                                               1671
```

Sequence ID No.: 5
Sequence length: 1437
Sequence type: Nucleic acid
Number of strands: Double-strand
Topology: Straight chain
Source:
Biological name: Perilla (Perilla frutescens)
Tissue type: Leaf
Direct source:
Library name: cDNA library
Clone name: p8R6
Sequence:

```
TTCAAAACTC ATAACGTGAT TGAGCTAATG TGCACATCTT CCTCTTCAAA GTCTACAGTG    60
TCATCCTACC AGCATCATCA TGATCAATCT CTTTATAATG AGGAGAATGG AGTAACAAGG   120
AGTGGGTTTT GTTACTCAGC TTCAACCTAC GTACGTACTA CTACTGACTC AACTCTCAAG   180
AGAATGAATA TAATATATAA TGGGCGATAG ATCTTTGTAG ATATGTAGGT GTAGCCTGCA   240
GGTGGTTAAT TAATTTCCGG TGTGGGAAAA TAAATAAATA AATAAATATA GCG ATG AGC   299
                                                          Met Ser
                                                            1
AGC AGC AGC AGC AGA AGG TGG AGA GAG AAT GAG GGG ATG CGA AGG ACA      347
Ser Ser Ser Ser Arg Arg Trp Arg Glu Asn Glu Gly Met Arg Arg Thr
          5                  10                  15
TTG CTG GGG TTG GGT TTG GGG CAG TTG GTT TCT TTC GAT TTG GCT ATC      395
Leu Leu Gly Leu Gly Leu Gly Gln Leu Val Ser Phe Asp Leu Ala Ile
     20                  25                  30
ATG ACC TTT TCT GCT TCT TTG GTT TCA ACC ACA GTG GAT GCA CCA CTT      443
Met Thr Phe Ser Ala Ser Leu Val Ser Thr Thr Val Asp Ala Pro Leu
 35                  40                  45                  50
ACT ATG TCG TTC ACT ACA TAC ACT GTT GTG GCC CTG CTC TAT GGA ACC      491
Thr Met Ser Phe Thr Thr Tyr Thr Val Val Ala Leu Leu Tyr Gly Thr
                 55                  60                  65
ATC TTG CTT TAC CGC CGC CAC AAA TTC TTG GTT CCA TGG TAC TGG TAT      539
Ile Leu Leu Tyr Arg Arg His Lys Phe Leu Val Pro Trp Tyr Trp Tyr
             70                  75                  80
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GCT CTC CTG GGG TTC GTG GAC GTC CAC GGC AAT TAT CTT GTT AAT AAA      587
Ala Leu Leu Gly Phe Val Asp Val His Gly Asn Tyr Leu Val Asn Lys
          85                  90                  95
GCA TTC GAG TTG ACA TCG ATT ACG AGT GTG AGC ATA CTG GAT TGT TGG      635
Ala Phe Glu Leu Thr Ser Ile Thr Ser Val Ser Ile Leu Asp Cys Trp
     100                 105                 110
ACA ATC GTG TGG TCC ATC ATC TTT ACA TGG ATG TTC CTA GGC ACA AAA      683
Thr Ile Val Trp Ser Ile Ile Phe Thr Trp Met Phe Leu Gly Thr Lys
115                 120                 125                 130
TAC TCT GTA TAC CAG TTT GTC GGT GCT GCT ATT TGT GTA GGA GGC CTC      731
Tyr Ser Val Tyr Gln Phe Val Gly Ala Ala Ile Cys Val Gly Gly Leu
                135                 140                 145
CTC CTC GTG CTT CTT TCC GAC TCA GGG GTC ACT GCT GCT GGT TCG AAT      779
Leu Leu Val Leu Leu Ser Asp Ser Gly Val Thr Ala Ala Gly Ser Asn
            150                 155                 160
CCT CTT TTG GGT GAT TTT CTT GTC ATA ACA GGC TCT ATT TTG TTC ACA      827
Pro Leu Leu Gly Asp Phe Leu Val Ile Thr Gly Ser Ile Leu Phe Thr
          165                 170                 175
CTC AGC ACT GTT GGT CAG GAA TAC TGC GTG AAG AGG AAA GAT CGT ATT      875
Leu Ser Thr Val Gly Gln Glu Tyr Cys Val Lys Arg Lys Asp Arg Ile
     180                 185                 190
GAA GTA GTA GCA ATG ATC GGT GTA TTT GGT ATG CTC ATC AGT GCA ACC      923
Glu Val Val Ala Met Ile Gly Val Phe Gly Met Leu Ile Ser Ala Thr
195                 200                 205                 210
GAG ATT ACT GTG CTG GAG AGG AAT GCC CTC TCA TCA ATG CAG TGG TCT      971
Glu Ile Thr Val Leu Glu Arg Asn Ala Leu Ser Ser Met Gln Trp Ser
                215                 220                 225
ACT GGA CTT TTG GCA GCC TAT GTT GTT TAT GCA CTG TCC AGC TTC CTC     1019
Thr Gly Leu Leu Ala Ala Tyr Val Val Tyr Ala Leu Ser Ser Phe Leu
            230                 235                 240
TTC TGC ACA CTC ACC CCT TTT CTT CTC AAG ATG AGT GGC GCT GCA TTT     1067
Phe Cys Thr Leu Thr Pro Phe Leu Leu Lys Met Ser Gly Ala Ala Phe
          245                 250                 255
TTC AAT CTT TCC ATG CTT ACA TCT GAT ATG TGG GCT GTT GCA ATT AGG     1115
Phe Asn Leu Ser Met Leu Thr Ser Asp Met Trp Ala Val Ala Ile Arg
     260                 265                 270
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ACA TTC ATA TAC AAC CAG GAG GTT GAT TGG TTA TAC TAT TTG GCC TTT    1163
Thr Phe Ile Tyr Asn Gln Glu Val Asp Trp Leu Tyr Tyr Leu Ala Phe
275                 280                 285                 290
TGT CTC GTT GTT GTT GGA ATA TTC ATA TAT ACA AAA ACA GAG AAG GAT    1211
Cys Leu Val Val Val Gly Ile Phe Ile Tyr Thr Lys Thr Glu Lys Asp
                295                 300                 305
CCT AAC AAT ACG AGA GCC CTT GAG AAT GGA AAC TTG GAT CAT GAA TAT    1259
Pro Asn Asn Thr Arg Ala Leu Glu Asn Gly Asn Leu Asp His Glu Tyr
            310                 315                 320
AGT CTC CTT GAG GAT CAA GAT GAC ACA CCA AGA AAA CCA TAGCTAGCTT     1308
Ser Leu Leu Glu Asp Gln Asp Asp Thr Pro Arg Lys Pro
        325                 330                 335
TGCCCACAAT CTTTTCATCA ACAGTTTTAA ATAATTCGTG AGGGGGAGAG AGATCGAGAT  1368
ACTAATTAAT GGACGTCTAT TATATAGTTG GAGGTTTTTG TTTTATTTAT TTATTTGAGT  1428
AAAAAAAAA                                                          1437
```

Sequence ID No.: 6
Sequence length: 2105
Sequence type: Nucleic acid
Number of strands: Double-strand
Topology: Straight chain
Source:
Biological name: Petunia
Tissue type: Leaf
Direct source:
Library name: cDNA library
Clone name: pSPGT1
Sequence:

```
AGTGAGCGCA ACGCAATTAA TGTGAGTTAG CTCACTCATT AGGCACCCCA GGCTTTACAC     60
TTTATGCTTC CGGCTCGTAT GTTGTGTGGA ATTGTGAGCG GATAACAATT TCACACAGGA    120
AACAGCTATG ACCATGATTA CGCCAAGCTC GAAATTAACC CTCACTAAAG GGAACAAAAG    180
CTGGAGCTCC ACGCGGTGGC GGCCGCTCTA GAACTAGTGG ATCCCCCGGG CTGCAGGAAT    240
TCCGTTGCTG TCGCCACAAT TTACAAACCA AGAAATTAAG CATCCCTTTC CCCCCCTTAA    300
AAAACATACA AGTTTTTAAT TTTTCACTAA GCAAGAAAAT ATG GTG CAG CCT CAT GTC  358
                                                Met Val Gln Pro His Val
                                                  1               5
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ATC TTA ACA ACA TTT CCA GCA CAA GGC CAT ATT AAT CCA GCA CTT CAA      406
Ile Leu Thr Thr Phe Pro Ala Gln Gly His Ile Asn Pro Ala Leu Gln
                10                  15                  20
TTT GCC AAG AAT CTT GTC AAG ATG GGC ATA GAA GTG ACA TTT TCT ACA      454
Phe Ala Lys Asn Leu Val Lys Met Gly Ile Glu Val Thr Phe Ser Thr
            25                  30                  35
AGC ATT TAT GCC CAA AGC CGT ATG GAT GAA AAA TCC ATT CTT AAT GCA      502
Ser Ile Tyr Ala Gln Ser Arg Met Asp Glu Lys Ser Ile Leu Asn Ala
        40                  45                  50
CCA AAA GGA TTG AAT TTC ATT CCA TTT TCC GAT GGC TTT GAT GAA GGT      550
Pro Lys Gly Leu Asn Phe Ile Pro Phe Ser Asp Gly Phe Asp Glu Gly
    55                  60                  65                  70
TTT GAT CAT TCA AAA GAC CCT GTA TTT TAC ATG TCA CAA CTT CGT AAA      598
Phe Asp His Ser Lys Asp Pro Val Phe Tyr Met Ser Gln Leu Arg Lys
                75                  80                  85
TGT GGA AGT GAA ACT GTC AAA AAA ATA ATT CTC ACT TGC TCT GAA AAT      646
Cys Gly Ser Glu Thr Val Lys Lys Ile Ile Leu Thr Cys Ser Glu Asn
            90                  95                  100
GGA CAG CCT ATA ACT TGC CTA CTT TAC TCC ATT TTC CTT CCT TGG GCA      694
Gly Gln Pro Ile Thr Cys Leu Leu Tyr Ser Ile Phe Leu Pro Trp Ala
        105                 110                 115
GCA GAG GTA GCA CGT GAA GTT CAC ATC CCT TCT GCT CTT CTT TGG AGT      742
Ala Glu Val Ala Arg Glu Val His Ile Pro Ser Ala Leu Leu Trp Ser
    120                 125                 130
CAA CCA GCA ACA ATA TTG GAC ATA TAT TAC TTC AAC TTT CAT GGA TAT      790
Gln Pro Ala Thr Ile Leu Asp Ile Tyr Tyr Phe Asn Phe His Gly Tyr
135                 140                 145                 150
GAA AAA GCT ATG GCT AAT GAA TCC AAT GAT CCA AAT TGG TCC ATT CAA      838
Glu Lys Ala Met Ala Asn Glu Ser Asn Asp Pro Asn Trp Ser Ile Gln
                155                 160                 165
CTT CCC GGG CTT CCA CTA CTG GAA ACT CGA GAT CTT CCT TCA TTT TTA      886
Leu Pro Gly Leu Pro Leu Leu Glu Thr Arg Asp Leu Pro Ser Phe Leu
            170                 175                 180
CTT CCT TAT GGT GCA AAA GGG AGT CTT CGA GTT GCA CTT CCA CCA TTC      934
Leu Pro Tyr Gly Ala Lys Gly Ser Leu Arg Val Ala Leu Pro Pro Phe
        185                 190                 195
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AAA GAA TTG ATA GAC ACA TTA GAT GCT GAA ACC ACT CCT AAG ATT CTT      982
Lys Glu Leu Ile Asp Thr Leu Asp Ala Glu Thr Thr Pro Lys Ile Leu
    200                 205                 210
GTG AAT ACA TTT GAT GAA TTA GAG CCT GAG GCA CTC AAT GCA ATT GAA     1030
Val Asn Thr Phe Asp Glu Leu Glu Pro Glu Ala Leu Asn Ala Ile Glu
215                 220                 225                 230
GGT TAT AAG TTT TAT GGA ATT GGA CCG TTG ATT CCT TCT GCT TTC TTG     1078
Gly Tyr Lys Phe Tyr Gly Ile Gly Pro Leu Ile Pro Ser Ala Phe Leu
                235                 240                 245
GGT GGA AAT GAC CCT TTA GAT GCT TCA TTT GGT GGT GAT CTT TTT CAA     1126
Gly Gly Asn Asp Pro Leu Asp Ala Ser Phe Gly Gly Asp Leu Phe Gln
            250                 255                 260
AAT TCA AAT GAC TAT ATG GAA TGG TTA AAC TCA AAG CCA AAT TCA TCA     1174
Asn Ser Asn Asp Tyr Met Glu Trp Leu Asn Ser Lys Pro Asn Ser Ser
        265                 270                 275
GTT GTT TAT ATA TCT TTT GGG AGT CTA ATG AAT CCA TCT ATT AGC CAA     1222
Val Val Tyr Ile Ser Phe Gly Ser Leu Met Asn Pro Ser Ile Ser Gln
    280                 285                 290
ATG GAG GAG ATA TCA AAA GGG TTG ATA GAC ATA GGA AGG CCG TTT TTA     1270
Met Glu Glu Ile Ser Lys Gly Leu Ile Asp Ile Gly Arg Pro Phe Leu
295                 300                 305                 310
TGG GTG ATA AAA GAA AAT GAA AAA GGC AAA GAA GAA GAG AAT AAA AAG     1318
Trp Val Ile Lys Glu Asn Glu Lys Gly Lys Glu Glu Glu Asn Lys Lys
                315                 320                 325
CTT GGT TGT ATT GAA GAA TTG GAA AAA ATA GGA AAA ATA GTT CCA TGG     1366
Leu Gly Cys Ile Glu Glu Leu Glu Lys Ile Gly Lys Ile Val Pro Trp
            330                 335                 340
TGT TCA CAA CTT GAA GTT CTA AAA CAT CCA TCT TTA GGA TGT TTT GTT     1414
Cys Ser Gln Leu Glu Val Leu Lys His Pro Ser Leu Gly Cys Phe Val
        345                 350                 355
TCT CAT TGT GGA TGG AAT TCA GCC TTA GAG AGT TTA GCT TGT GGA GTG     1462
Ser His Cys Gly Trp Asn Ser Ala Leu Glu Ser Leu Ala Cys Gly Val
    360                 365                 370
CCA GTT GTG GCA TTT CCT CAA TGG ACA GAT CAA ATG ACA AAT GCC AAA     1510
Pro Val Val Ala Phe Pro Gln Trp Thr Asp Gln Met Thr Asn Ala Lys
375                 380                 385                 390
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CAA GTT GAA GAT GTG TGG AAA AGT GGA GTA AGA GTG AGA ATA AAT GAA      1558
Gln Val Glu Asp Val Trp Lys Ser Gly Val Arg Val Arg Ile Asn Glu
                395                 400                 405
GAT GGT GTT GTT GAA AGT GAG GAA ATC AAA AGG TGT ATT GAA TTG GTA      1606
Asp Gly Val Val Glu Ser Glu Glu Ile Lys Arg Cys Ile Glu Leu Val
            410                 415                 420
ATG GAT GGA GGA GAG AAA GGG GAA GAA TTG AGA AAG AAT GCT AAG AAA      1654
Met Asp Gly Gly Glu Lys Gly Glu Glu Leu Arg Lys Asn Ala Lys Lys
        425                 430                 435
TGG AAA GAA TTG GCT AGA GAA GCT GTG AAG GAA GGT GGA TCT TCA CAC      1702
Trp Lys Glu Leu Ala Arg Glu Ala Val Lys Glu Gly Gly Ser Ser His
    440                 445                 450
AAG AAT TTA AAG GCT TTT ATT GAT GAT GTT GCC AAA GGG TTT TAATATTTAC  1754
Lys Asn Leu Lys Ala Phe Ile Asp Asp Val Ala Lys Gly Phe
455                 460                 465         468
AGGCTTTTGC CGTGATATTA CTTCCCCTAG TTGGCGATTC ACTCTTTGTG GACTTGCTTG   1814
ACAAAAAACT GAGGGAATGT GCTAAGACAC GCTAATGCTT TAAGAAGTCA TTTCCAAGGC   1874
TTGAAGCCTG CTTTTAAAAC TTATTAGCCA GTAATCTATA GGGTTCTCTT CTATTTTTCT   1934
CTGTCTCTCT TTTTAGCCTT TTTCTTTCCA AGGTTTAAGA ATAGCGTGAA CATAGCTTAG   1994
TACGTAGTCT TGGTATCTCT ATCTTACCAA GTGCAAGATT ATGCTTATGC TGTCCTCCTA   2054
AATTTCTTAA TAAAATGCAA GATGAAAAAG TACAAAAAAA AAAAAAAAAA A            2105
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Declaration and Power of Attorney For Patent Application

特許出願宣言書及び委任状

Japanese Language Declaration

日本語宣言書

下記の氏名の発明者として、私は以下の通り宣言します。

As a below named inventor, I hereby declare that:

私の住所、私書箱、国籍は下記の私の氏名の後に記載された通りです。

My residence, post office address and citizenship are as stated next to my name.

下記の名称の発明に関して請求範囲に記載され、特許出願している発明内容について、私が最初かつ唯一の発明者（下記の氏名が一つの場合）もしくは最初かつ共同発明者であると（下記の名称が複数の場合）信じています。

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled

GENE CODING FOR A PROTEIN HAVING GLYCOSIDE TRANSFER ACTIVITY

上記発明の明細書（下記の欄でx印がついていない場合は、本書に添付）は、

the specification of which is attached hereto unless the following box is checked:

☐ __月__日に提出され、米国出願番号または特許協定条約国際出願番号を_____とし、
（該当する場合）_____ に訂正されました。

☒ was filed on July 16, 1998
as United States Application Number or
PCT International Application Number
PCT/JP98/03199
and was amended on
_____
(if applicable).

私は、特許請求範囲を含む上記訂正後の明細書を検討し、内容を理解していることをここに表明します。

I hereby state that I have reviewed and understand the contents of the above identified specification, including the claims, as amended by any amendment referred to above.

私は、連邦規則法典第３７編第１条５６項に定義されるとおり、特許資格の有無について重要な情報を開示する義務があることを認めます。

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I hereby claim foreign priority under Title 35, United States Code, Section 119 (a)-(d) or 365(b) of any foreign application(s) for patent or inventor's certificate, or 365(a) of any PCT International application which designated at least one country other than the United States, listed below and have also identified below, by checking the box, any foreign application for patent or inventor's certificate, or PCT International application having a filing date before that of the application on which priority is claimed.

Prior Foreign Application(s)
外国での先行出願

(Number) (番号)	(Country) (国名)	(Day/Month/Year Filed) (出願年月日)	Priority Not Claimed 優先権主張なし
9-200571(Pat. Appln.)	Japan	25/July/1997	☐
			☐

私は、第３５編米国法典１１９条(e)項に基いて下記の米国特許出願規定に記載された権利をここに主張いたします。

I hereby claim the benefit under Title 35, United States Code, Section 119(e) of any United States provisional application(s) listed below.

(Application No.) (出願番号)	(Filing Date) (出願日)	(Application No.) (出願番号)	(Filing Date) (出願日)

私は、下記の米国法典第３５編１２０条に基いて下記の米国特許出願に記載された権利、又は米国を指定している特許協力条約３６５条(c)に基ずく権利をここに主張します。また、本出願の各請求範囲の内容が米国法典第３５編１１２条第１項又は特許協力条約で規定された方法で先行する米国特許出願に開示されていない限り、その先行米国出願書提出日以降で本出願書の日本国内または特許協力条約国際提出日までの期間中に入手された、連邦規則法典第３７編１条５６項で定義された特許資格の有無に関する重要な情報について開示義務があることを認識しています。

I hereby claim the benefit under Title 35, United States Code, Section 120 of any United States application(s), or 365(c) of any PCT International application designating the United States, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application in the manner provided by the first paragraph of Title 35, United States Code Section 112, I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, Section 1.56 which became available between the filing date of the prior application and the national or PCT International filing date of application.

(Application No.) (出願番号)	(Filing Date) (出願日)	(Status: Patented, Pending, Abandoned) (現況：特許許可済、係属中、放棄済)

私は、私自身の知識に基ずいて本宣言書中で私が行なう表明が真実であり、かつ私の入手した情報と私の信じるところに基ずく表明が全て真実であると信じていること、さらに故意になされた虚偽の表明及びそれと同等の行為は米国法典第１８編第１００１条に基ずき、罰金または拘禁、もしくはその両方により処罰されること、そしてそのような故意による虚偽の声明を行なえば、出願した、又は既に許可された特許の有効性が失われることを認識し、よってここに下記のごとく宣誓を致します。

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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Japanese Language Declaration
(日本語宣言書)

委任状： 私は下記の発明者として、本出願に関する一切の手続きを米特許商標局に対して遂行する弁理士または代理人として、下記の者を指名いたします。（弁護士、または代理人の氏名及び登録番号を明記のこと）

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